### STIC-Biotech/ChemLib

From:

Yu, Misook

Sent: To:

Wednesday, August 28, 2002 8:35 AM STIC-Biotech/ChemLib 09/900,147

Subject:

Please search SEQ ID NO:1

Examiner Misook Yu, Ph.D. 703-308-2454 (Phone) Art Unit 1642 CM1-8E18 (Room) CM1-8E12 (Mail Box)

**Edward Hart** Technical Info. Specialist STIC/Biotech CMI 6802 Tel: 305-9203

All Slauch here

	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher:	NA Sequences:	STN:
Phone:	AA Sequences:	DIALOG:
Location:	Structures:	Questel/Orbit:
Date Picked Up: 100 (AZ)	Bibliographic:	DRLink:
Date Completed:	Litigation:	Lexis/Nexis:
Searcher Prep/Review:	Full text:	Sequence Sys.:
Clerical:	Patent Family:	WWW/Internet:
Online time:	Other:	Other (specify):

Title: Perfect score: Sequence:

US-09-900-147-1

Scoring table:

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Post-processing: Minimum Match Maximum Match Listing first

Database

SPTREMBL\_19:\*

1: #p\_archea:\*

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Copyright (c) 1993 - 2000 Compugen
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09627 brugia mala
044080 drosophila
090600 drosophila
090654 homo sapian
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091267 arabidopsis
091275 arabidopsis
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      macaca fasc
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RESIDENCE FROM N.A.

RAMAI J., Shibagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Kawai J., Shibagawa A., Shibata K., Ronon H., Rasukawa T., Sulto R.,

RA Kawaa K., Izawa M., Nighi K., Riyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Aghibata M., Batalov B., Casawant T.,

RA Saito T., Okazaki Y., Ashibatara M., Batalov B., Casawant T.,

RA Schrint. K., Matsuda H.A., Ashibatara M., Batalov B., Kochiwa H.,

RA Schrint. M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schrint. M., Okado T., Furuno M., Anno H., Baidarali R., Barsh G.,

RA Schrint. M., Okado T., Furuno M., Anno H., Baidarali R., Barsh G.,

RA Biaka J., Boffelli D., Bojunga N., Carninci P., de Bonsido M.F.,

RA Schrint. M., Okado T., Furuno M., Anno H., de Bonsido M.F.,

RA Biaka J., Baffelli D., Bojunga N., Carninci P., de Bonsido M.F.,

RA Hordone P., Ring B., Ringvaid M., Hume D.A., Waniya H., Lee N. H.,

RA Hordone P., Ring B., Ringvaid M., Rodriguez I., Sakamoto N.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Rawaji H., Rohtsuki S.,

RA Hordone P., Schochbach C., Seys T., Shibata Y.,

RA Hordone P., Schochbach C., Seys T., Shibata Y.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Rawaji H., Rohtsuki S.,

RA Hayashizaki Y.,

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RA Hayashizaki Y.,

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Eukaryota: Metazos; Chordata; Craniata; Vartabrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
MCBI_TaxID=10090;
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Opbz44 homo sapiam
Opbz45 homo sapiam
Opfra5 oryza sativ
Opfra6 arabidopsis
Opfra6 arabidopsis
Opfra7 arabidopsis
Opfra7 arabidopsis
Opfra7 homo sapiam
Opfra8 arabidopsis
Opfra9 arabidopsis
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Result

Score

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Query Match

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RESULT 3
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ID Q9UG28
AC Q9UG28
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RECEINE-2108560; PubMed-11217851;

RA NAMEDILINE-2108560; PubMed-11217851;

RA NAMEDILINE-2108560; PubMed-11217851;

RA ALABAWA T., HAMA A., FIKUMISHI Y., KONDO H., Adachi J., FOKUda S.,

RA ALABAWA T., HAMA A., FIKUMISHI Y., KONDO H., ROOMO S., Tamanaka I.,

RA ALABAWA T., IZAWA M., MISHI Y., KIYOSAWA H., ROOMO S., Tamanaka I.,

RA ALABAWA T., OKABAH Y., GOJOBOTI T., BOND H., RESUKAWA T., Seito R.,

RA ALABAWA T., RAMA H., MISHI Y., RING B., KOCHIWA H.,

RA KABOLA K., MALSUD Y., MIKAIMO I., PEGOLE G., QUACKENDUSH J.,

RA KUCHI P., LEWIS S., HALSUD Y., NIKAIMO I., PEGOLE G., QUACKENDUSH J.,

RA SCHIIMI L.M., SLAUDII P., SUZUKI R., TOMILE M., HOGNEF L., MASHIO T.,

RA SCHIMI L.M., SLAUDII P., SUZUKI R., TOMILE M., HOGNEF L., BAFSH G.,

RA BIAME J., BOITELI D., BOJUNGS N., CARTINCI P., do BONALO M.F.,

RA BIAME J., BOITELI D., BOJUNGS N., CARTINCI P., do BONALO M.F.,

RA BIAME J., BOITELI D., BOJUNGS N., CARTINCI P., do BONALO M.F.,

RA BIAME J., BOITELI D., BOJUNGS N., CARTINCI P., do BONALO M.F.,

RA BIAME J., BOITEL C., PIECCHET C., PUJISA M., GATIBOIDI M.,

RA KUCHI P., SELONI J., HOSMIN M., HUMB D.A., KAMBUS M., LEG N.H.,

RA KOMONIS P., MARCHIONNI L., MASHIMS J., MEZIATOLII J., NOMBARTIS P.,

RA KOMONIS P., MARCHIONNI L., MASHIMS J., MEZIATOLII J., KOMBARTIS P.,

RA KOMONIS P., MARCHIONNI L., MASHIMS J., MEZIATOLII J., KOMBARTIS P.,

RA KUCHI P., SELONI R., NOSHIGA K., MESGSAWA T., KANGATI, K., KONEGUKI S.,

PLANTA P., MARCHINI S., MASHIMS T., KANGATI, K., KONEGUKI S.,

PLANTA P., MARCHINI S., MASHIMS T., KANGATI, K., KONEGUKI S.,

PLANTA P., MARCHINI S., MASHIMS T., KANGATI, K., KONEGUKI S.,

PLANTA P., MARCHINI S., MASHIMS T., KANGATI, K., KONEGUKI S.,

PLANTA P., MARCHINI S., MASHIMS T., KANGATI, K., KONEGUKI S.,

PLANTA B., MARCHINI S., MASHIMS T., KANGATI, K., KONEGUKI S.,

PLANTA P., MARCHINI S., MASHIMS T., KANGATI N., KONEGUKI S.,

PLANTA P., MARCHINI S., MASHIMS T., KANGATI N., KONEGUKI S.,

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01-JUN-2001 (TEMBLIEL 17
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7 01-DEC-2001 (TEMBLIEL 17
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Best Local Similarity 100.0%;
Matches 37; Conservative (
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   09UC28;
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Functional annotation of a full-length mouse EDNA collection.";

Nature 409:685-690(2001).

EMBL; AK019997: BAB31959.1; -.

HSSP; Q14188; 1CF7.

HGD; MGI:010314; Tfdp1.

InterPro; IPR003316; ESF_TDP:

Pfam; PF03319; EZF_TDP; 1.

Pfam; PF03319; EZF_TDP; 1.

SEQUENCE 396 AA; 43804 MM; 392AE2ED28165622 CRC64;
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Eukaryota; Metazoa;
Nammalla; Eutherla;
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Interpro; IPRO03316; E2F_TDP.
Pfam; PPO0319; E2F_TDP; 1.
SEQUENCE 290 AA; 32494 MF; AA3079A6FC4F1DD0 CRC64;
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STRAIN-CS7BL/6J; T
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Rodentia;
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Pred. No. 4.9e-18;
; Mismatches 0;
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Pred. No. 3.5e-18;
Hismatches 0;
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01-JUN-2001 (Tr
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Query Match 90.3%;
Best Local Similarity 88.9%;
Matches 32; Conservative
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Best Local Similarity 100.0%;
Watches 37; Conservative C
                                                                                                           *Brugia malay! DP1 transcription for Submitted (JUL-2000) to the EMBL/G EMBL, Apple 340; AACI2473.1; - AACI2473.1;
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01-MAR-2001 (TERMBLES). 19, Las
01-DEC-2001 (TERMBLES). 19, Las
TRANSCRIPTION FACTOR DP1.
Brugia malayi.
Eukaryota Metazoa; Nematoda; C
Onchocercidae; Brugia.
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09GT27;
01-MAR-2001
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01-MAY-2000 (TrEMBLiel. 13, Last sequence up
01-JUN-2001 (TrEMBLIEL. 17, Last annotation
HYPOTHETICAL 46.0 KDA PROTEIN (FRAGMENT).
DRFLP4346232.
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Ansocre H., Wirkner D., Neves H.W., Gassenhuber J., Wiemann S.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ.detabases.
EMBL; AL080205; CA345775.1; ".
HSSP; Q14188; ICP7.
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Eukaryota: Metazoa:
Mammalia: Eutheria;
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SEQUENCE: 416 AA; 4
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Dissanayake S.;
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Pfam; PF02319; E2F_TDP; 1:
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Primates;
      ; Score 169; DB
; Pred. No. 1.2e
3; Mismatches
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EMBL/GenBank/DOBJ databases
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Pred. No. 5.1
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5.1e-18;
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L.28-15;
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(TrEMBLrel. 05, Created)
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N FACTOR DP (FRAGMENT).

PRELIMINARY;

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OSVÉMO PRELIMINARY; PRT; 445 AA.

AC OSVÉMO; O17472;
DT 01-MAY-2000 (TEEMBLTel. 13, Created)
DT 01-MAY-2000 (TEEMBLTel. 13, Last sequence update)
DT 01-JUN-2000 (TEEMBLTel. 17, Last annotation update)
DT 01-JUN-2001 (TEEMBLTel. 17, Last annotation update)
DE DP GENE PRODUCT (TRANSCRIPTION PACTOR E2F DP SUBUNIT).

GN DP OR CG4654.
OS DICOSOPHILA melanogaster (Fruic fly).
OS ENHATYOLS; Mecasos, Arthropoda; Trachesta; Hexapoda; Insecta;
C Pterygota; Neoptexa; Endopterygota; Diptera; Brachycera; Muscomorpha;
C Ephydroidea; Drosophilidae; Drosophila.

NEDI_TaxID-7227;
NEDI_TaxID-7227;
              용
RX Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Galle R.F.
RA Adams M.D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.
RA Amanatides P.G., Scharer S.E., Li P.W., Hoskins R.A., Galle R.F.
RA Mannatides P.G., Scharer S.E., Li P.W., Hoskins R.A., Galle R.F.
RA Amanatides P.G., Scharer S.E., Li P.W., Hoskins R.A., Galle R.F.
RA George R.A., Levis S.E., Richards S., Ashburing, M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhanga, M., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Ashbyani A., An H. J., Andrews Pfennkoch C., Miklos G.L.G.,
RA Abril J.F., Ashbyani A., An H. J., Andrews Pfennkoch C., Baldwin D.,
RA Beson K.Y., Benos P.V., Berman B.F., Bhandari D., Bolshakov S.,
RA Beson K.Y., Benos P.V., Berman B.F., Shandari D., Botcher D.,
RA Beson K.Y., Benos P.V., Berman B.F., Shandari D., Botcher P.,
RA Borkova D., Botchan M.R., Bouck J., Barokstein P., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherris R.C., Busham D.A., Butler H., Davies P.,
RA Cherris R.C., Busham D.A., Downes M., Dugays A.D., Dev I., Dietz S.M.,
RA Glodek A., Gong Y., Gorrell J.M., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Weil M. H., Toegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravit S., Kulp D., Lai Z.,
RA Hostin D., Klishina N.V., Mobarey C., Morris J., Moshrefl A.,
RA Holt N., Wattel B., McIntosh T.C., McLeed M.P., McPherson D.,
RA Hount S.M., Holland R.S., Mixon K., Nusskern D.R., Paclab J.M.,
RA Holton D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Holton D.R., Paclab J.M.,
RA Holton D.R., Paclab J.M.,
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Best Local Similarity 86.1%;
Matches 31; Conservative
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EMBL; AF01152; ALB897765.1; ..
BUSE; AV01152; ALB897765.1; ..
BUSE; Q14188; LCF7.
FlyBase; PBgn0011763; Dp.
InterPro; IPF003316; E2F_TDP.
Pfam; PF02119; E3F_TDP; 1.
BOM TEP
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DP OR CG4554.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Nuscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
MCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BERKELEY;
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Pred. No. 3e-15;
4; Mismatches 1
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A DUTONIO R.J., BONNETCE P.C., O'FBATTELL P.H.;

A DUTONIO R.J., BONNETCE P.C., O'FBATTELL P.H.;

A DUTONIO R.J., BONNETCE P.C., O'FBATTELL P.H.;

AND HELLORS OF the Drocophila dDp, dE2F, and cyclin E genes reveal

ATT the G1-S transition.*;

AND L. CELL. Biol. 18:141-151(1998).

BE MBL; AE003819; AAF58403.1; -.

BMBL; AE003819; AAF68403.1; -.

BMBL; AF031700; AAC02771.1; -.

        Query Match
Best Local S
Matches 33
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Best Local Similarity 85.1
Matches 31: Conservative
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OSM254
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The genome sequence of Drosophila melanogaster.*;
Science 287:3165-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #CA661.

Homo sepiens (Human).

Eukaryota: Hetasca: Chordata: Craniata: Vertebrata: Eutaleostomi:

Hommalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
                                                                                                                                                                                  Pang X., Vaughan H., Chen W., StClair P., Han K., Cebon J.;
"Cloning and character@fation of novel genes related to hepatocellular carcinoma.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF219119; AAP37562.1;
EMBL; AF219119; AAP37562.1;
InterPro: TRR00316; EZP_TDP.
Pfam: PP02319; EZP_TDP: 1.
SEQUENCE 233 AA; 26053 MM; CSP9F8D2B7384794 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-61 FROM N.A.
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Similarity 86.5%;
32; Conservative
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Last sequence update)
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Pred. No. 3.7e-15;
4; Mismetches 1
Score 164; DB
Prad. No. 3.6e
3; Mismatches
             DB 4: [
:.6e-15;
BB 2;
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                                                                                  Length 233;
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Best Local Similarity 83.3%;
Matches 30; Conservative
                                               Ouery Match 81.2%;
Best Local Similarity 83.3%;
Natches 30; Conservative
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FEBS Lett. 486:79-87(2000).

EMBL: A.724532; CAC15484.1; -.

HSSP: 014188; ICF7.

INCEPTO: IPRO0316; E2F_TDP.

PÉAM; PEO2319; E3F_TDP; 1.

SECUTENCE 385 AA; 42755 MM; 51
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OSPNY2;
OPENY2;
OL-MAR-2001 (TrEMBLrel. 1
OL-MAR-2001 (TrEMBLrel. 1
OL-DEC-2001 (TrEMBLrel. 1
DP-LIKE PROTEIN.
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O912E7
O912E7
O1-OCT-2000 (TERRIFE). 15, Created)
O1-OCT-2000 (TERRIFE). 15, Last sequence update)
O1-DCC-2001 (TERRIFE). 19, Last annotation update
TRANSCRIPTION FACTOR-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliama (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicota; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TexID-3703;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Bevan M., Pohl T., Weizenegger
Lencke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-20562805; PubMed-11108847;
Mayar E., Atanassovs A., de Veylder L., Rombauts S., Inze D.;
"Characterization of two distinct DP-related genes from Arabidopsis
                                                                                                                 HSSP: Q14188; ICF7.
InterPro; IPR003316; E2F_TDP.
Pfom; PF02319; E2F_TDP; 1.
SEQUENCE 413 AA; 45604 MW;
                                                                                                                                                                     EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/G
EMBL: AL162751; CAB83299.1; .
                                                                                                                                                                                                                                                                                                                       Arabidoppis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sparmatophyta; Magnoliophyta; eudicotyledons; cgre eudicots; Rosideursids II; Brassicales; Brassicaceae; Arabido
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16, Last sequence update)
19, Last annotation update)
                                               Score 151; DB 10;
Pred. No. 4.5e-13;
3; Mismatches 3;
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Pred. No. 4.1e-13;
3; Wismatches 3;
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                                                                                                                                                                                      EMBL/GenBank/DDBJ
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                                                                                                                  239FDC6DAED2F7:23
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                                                                                                                     CRC64;
                                                                          Length 413:
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Best Local Similarity 75.8%;
Matches 25; Conservative
       Query Match
Best Local Similarity
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EU Arabidopais sequencing project;
EU Arabidopais sequencing project;
Submitted (APR-2000) to the EMBL/Gen
EMBL; ALL6291; CABB9984.1; ~.

HSSP; 014188; LCE7;
InterPro; 1PR003116; E2F_TDP,
Pfam; PP02319; E3F_TDP; 1.

SEQUENCE 288 AA; 13560 MM; ECOAD
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Sequence
                                                                                                                                                                                                                                   Arabidopais thaliana (Mouse-ear cress).
Eukeryote: Yiridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicalegg Brassicacese; Arabidopsis.
NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DP-LIKE PROTEIN (EC 6.3.2.19)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledona; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-0CT-2000 (TrEMBLrel. 15, Las
01-DEC-2001 (TrEMBLrel. 19, Las
DP-2 TRANSCRIPTION FACTOR-LIKE
                                                                                   PRBS Lett. 486:79-87(2000).
EMBL, AZ294531; CAC13483.1;
HSSP: Q14188; 10F7.
InterPro; IPRO03316; E2F_TDP.
Pfam; PF02319; E2F_TDP; 1.
                                                                                                                                                                     SEQUENCE FROM N.A. MEDILINE-20562805; PubMed=11108847; MEDILINE-20562805; PubMed=11108847; Mayar E., Rombauts S., Mayar E., Kansseova A., de Yeylder L., Rombauts S., "Characterization of two distinct DP-related genes fro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-3702;
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                                                             ξ
                                                             33038 MW;
         73
       .80
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; Pred. No. 4e-1
6; Mismatches
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         Score
                                                             644324E13561FEC5
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       136; DB 10;
No. 4.1e-11;
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Indels

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Length

CRC64;

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Length 292,

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RESULT
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Best Local 5
Matches 24
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Query Match
Best Local Similarity
                                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 21394624; PubMed-11463372;

Ceol C.J., Horvitz H.R.;

'dpl-1 DP and delt-1 E2F Act with lin-35 Rb

1n C. elegans vulval Development.";

Hol. Cell 7:461-473(2001).

EMBL: AY028167; AAK19023.1; -

EMBL: AY028167; AAK19023.1; -

HSSP: Q16254; 1CF7.

InterPro: IPRO03116; E2F_TDP;

InterPro: IPRO03116; E2F_TDP;

SEQUENCE 287 AA; 32373 MM; 434446E88F
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09FET1;
01-MAR-2001
01-MAR-2001
01-DEC-2001
DP PROTEIN.
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01-JUN-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Remirez-Parre E., Gutlerrez C.;
"Characterization of wheat DP, a heterodimedization partner of the
plant EZF transcription factor which stimulates E2FIDNA binding.";
FBS Latt. 486:73-78(2000).
EMBL: AJ271917: CAC19034.1;
EMBL: AJ271917: CAC19034.1;
INterPro: 17PR00316: E2F_TDP.
Pfam: PF0319: E2F_TDP: 1.
SEQUENCE 261 AA: 29262 NM: 5008DBF193163A28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triticum ap.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae; Pooideae;
Triticeae; Triticum,
                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota: Hetazos; Nematoda: Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        931E8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20562804; PubMed-11108846;
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                                                                                                                                                                                                                                                                                                 NCBI_TaxID-6239;
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KNIRRRYYDALNYFWALDIIARDKKEIKWKGLP 135
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1 (TrEMBLrel. 16,
1 (TrEMBLrel. 19,
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(TrEMBLIE).
(TrEMBLIE).
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75.01;
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19,
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Pred.
  Score 82.5; DB 5; Pred. No. 0.0014;
                                                                            4344445E86E8C7A8 CRC64;
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. No. 9.6e-11;
ismatches 2;
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                     Length 287;
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Best Local Similarity 50.0
Matches 17; Conservative
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                                                                            SEQUENCE FROM N.A.

TISSUE-TEMPORAL LOBE RIGHT;
OBAGA N., HIGA M., Kusuda J., Tanuma R., Is
SUEUKI Y., Sugano S., Hashimoto K.?
TISOLATION of full-length cDNA clones from
libraries. ";
Submitted (APR-2001) to the EMBL/GenBank/DD
EMBL; AB060895; BAB46898.1; ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            090289
                                                                                                                                                                                                                                          Q95KG1 PRELIMINARY; PRT; 281 AA.
Q95KG1;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel.) 19, Last annotation update)
HYDOTHETICAL 31.7 TOA ##DOTEIN
HACAGA fascicularis (C7ab sating macaque) (Cynomolyus monkey).
HACAGA fascicularis (C7ab sating macaque) (Cynomolyus monkey).
HAMMALIS; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Investigating biology.*;
Science 383:3012-3018(1998).
Science 383:3012-3018(1998).
BMBL; ALL17303; CAS60421.1;
HSSP; Q10254; 1CF7.
HSSP; Q10254; 1
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Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinse; Caenorhabditis.
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NEDLINE-99069613; PubMed-9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1999)
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                                          Hypothetical sequence 2
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71 KRRYYDYINYLEGLGYVEKVEKNNIRWIGDNNNS 104
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Pred, No. 0.0021;
5; Mismatches 11;
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                                              PD71A9F7C2EEE0E5 CRC64;
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Higal M., Terao

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Rhabditoidea;

Ouery Match 39.0%; Score 72.5; Dn 6; Length 281; Best Local Similarity 48.3%; Pred. No. 0.036; Matches 14; Conservative 7; Mismatches 7; Indels 1; Gaps 1.

Search completed: August 28, 2002, 13:03:00 Job time: 221 sec

7itle: Perfect score: Sequence:

US-09-900-147-1 186

Scoring table:

BLOSUH62

Gapop 10.0 , Gapext 0.5

Meximum DB

seq length: 0 seq length: 20000000000

Database :

÷ :: 22 :: PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

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Post~processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  August 28, 2002, 12:57:49; Search time 18.36 Seconds (without alignments)
193.644 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen
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CrSpecies: Nus musculus (house mouse)
CrSpecies: Nus musculus (house mouse)
CrSpecies: 11-Nov-1994 facequence_revision 11-Nov-1994 attext_change 10-Dec-1999
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CrDctes: 11-Nov-1994 facequence 11-Nov-1994 attext_change 10-Dec-1999
A:Fille: Heterodimerization of the transcription factors E2F-1 and DF-1 leads to call reference number: A48585; MUID:94010284
A:Accession: B48985
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptu A:Holecule type: mRNA
A:Residues: 1-410 chell.
A:Residues: 1-410 cirr
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A: Status; preliminary
A: Holecule type: mRNA
A: Residues; 388-410 <6212>
A: Cross-references: EMBL: x72310
A: Cross-references: EMBL: x72310
C: Superfamily: transcription factor DP
C: Keywords: DNA binding: transcription factor
transcription factor DP-1 - human C;Species: Homo sapiens (man) C;Date: Il-Nov-1994 *text_change 10-Dec-1999 C;Date: Il-Nov-1994 *text_change 10-Dec-1999 C;Accession: A48585 R;Helin, K.; Hu, C.L.; Fattaey, A.R.; Lees, J.A.; Dynlacht, B.D.; Ngwu, C.; Harlow Genes Dev. 7, 1850-1861, 1993
                                                                                                                                                                                                                       RESULT
A48585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Overy Match 100.01; Score 186; DB 3; Best Local Similarity 100.01; Pred. No. 9.38-18; Matches 37; Conservative 0; Mismatches 0;
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A;Gene: GDB:TFDP2; DP2
A;Cross-references: GDB:638814
A;Mare position: J923-3q23
A;Mare: DKF2p434G22.1
C;Superfamily: transcription factor DP
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A:Reference number: 217537
A:Reference T12511
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A;Status: preliminary; nucleic acid sequence not shown
A;Status: type: mRNA
A;Rosidues: 1-410 <BEL>
A;Rosidues: 1-410 <BEL>
A;Cross-references: GB:L33959; NID:g414316; PIDN:AAA58440.1; PID:g414317
C;Superfanity: Cranscription factor DP
C;Reywords: DNA binding; transcription factor
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N/Alternate names: EIP dimerization partner 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIZHANG, Y.; Chellappan, S.P.
Dhoogene 10, 2085-2093, 1995
NITLLE: Closing and characterization of human DP2, a novel
NReference number: 137297; MUID:95303470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: EMBL:ALD80206; Cross-references: EMBL:ALD80206; Experimental source: adult testis; clone DKF2p434G222; Experimental source: adult testis; clone DKF2p434G222; Alba C.L.; Eukerberg L.R.; Ngwu, C.; Harlow, E.; Lees, J.A. (ol. Cell. Blo). 15, 2536-2546, 1995. Harlow, E.; Lees, J.A. (ol. Cell. Blo). 15, 2536-2546, 1995 and DF family proteins. 171616-7999 and DF family proteins. 171616-79999 and DF family proteins.
                                                                                Query Hatch
Best Local S
Matches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Cross-references: GB:L40386; NID:g703084; PIDN:ANA69016.1; PID:g703085; Phang, Y.; Chellappan, S.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :Status: preliminary
;Molecule type: mRNA
;Residues: 'H',33-416 <NUA>
                                                                                                                                                                                                                                                                                                                                                                     Cross-references: SMBL: U35117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Homo sapiens (man)
Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 17-Nov-2000
Accession: T12511: A57381: 137297: 139180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary; translated from GB/RMBL/DDBJ Holecule type: mRNA Residues: 'M', 33-49 <2HAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary; translated from GB/EMBL/DDBJ MoLecule type: mRNA
Residues: "W, 33-149,"(),",144-416 <ZHAl>
Cross-references: EMBL:U18422; NID:9604478; PIDN:AAB60378.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 KNIRRRYYDALHYLMAMNIISKEKKEIKWIGLPTNSA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KNIRRRYTDALMYLMAMNIISKEKKEIKWIGLPTNSA 3:
1 KNIRRRYYDALWYLMANNIISKEKREIKWIGLPTNSA 37
                                                                                37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-416 <ANS>
                                                                       100.0%; Score 186; DB 2: Length 416; librity 100.0%; Pred. No. 5.4e-18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 186; DB 2;
100.0%; Pred, No. 5.3e-18;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                     NID:g1008545; PIDN:AAC50642.1; PID:g1008546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dimerization partner of E2F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID: 9604479
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                                                                          Caps
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A;Cross-references: FlyBase:FBgn0011763
C;Superfamily: transcription (actor DP
                       hypothetical protein 73367.1 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C:Accession: T25207 # R:Barlow, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             용
                                                                                                                                                       RESULT
T25207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    유
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A; Residues: 1-429 <GIRl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArAccession: $34572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross references:
ubmitted to the EMBL Data Library, December 1995
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 86.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Metch 100.0%; Score 186; DB 3; Best Local Similarity 100.0%; Prod. No. 5.60-18; Matches 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: B55745
                                                                                                                                                                                                                                                                145 KNIRRRYDALNYLMAINVISKDKKEIRWIGLPANS 180
                                                                                                                                                                                                                                                                                           1 KNIRRRYKDALNYLMAMNIISKEKKEIKHIGLETNS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KNIRRRYYDALNYLJAJNNIISKEKKEIKWIGLPTNSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB: x79700; NID: g516866;
                                                                                                                                                                                                                                                                                                                                                                                          89.24;
                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Score 166; DB 2;
Pred. No. 2.9e-15;
                                                                          15-Oct-1999 #text_change 15-Oct-1999
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## 148 KNIRRRYDALNYLWAMNIISKEKKEIKWIGLPTNSA 184

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transcription factor DRFF1 chain 1 - mouse
N;Alternate names: transcription factor DP-1
C;Species: Mus musculus (house mouse)
C;Decies: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 10-Dec-1999
C;Accession: $30049; $34572
C;Accession: $30049; $34572
R;GIT11ng, R.: Partridge, J.F.; Banders, L.R.; Burden, N.; Totty, N.F.; Hauan, J.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type; protein
A; Residues: 75-90; 111-131, 164-184; 191-207; 235-249; 281-293; 302-313; 321-328 <GJR2>
C; Superfently: transcription factor DP
C; Reywords: DNA binding; transcription factor
F; 84-204/Domain: DNA binding #status predicted <DNA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: A new component of the transcription factor DRTF1/E2F A; Reference number: $30049; MUID:93188967.
A; Accession: $30049
                                                                                                                                      RiDynlacht, B.D.; Brook, A.; Dembski, M.; Yenush, L.; Dyson, M. Proc. Natl. Acad. Sci. U.S.A. 91, 6359-6363, 1994
A;Title: DNA-binding and trans-activation properties of Drosophila A;Reference number: A55745; MUID:94394381
A;Accession: B55745
                                                                                                                                                                                                                                                                                                                                                                            transcription factor DP - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                            Species: Drosophila melanogaster
Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 KNIRRYTDALMYLMAMNIISKEKKEIKHIGLPINSA 199
P1D: 9516867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 429;
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Length 377

Indels

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Caps

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A;Map position: 5
A;Introns: 84/3; 128/1; 142/3; 163/3; 212/3; 249/1; 279/3; 303/2
A;Note: P122.160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription factor-like protein - Arabidopsis chaliana
N;Alternate names: protein F1264.160
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: 748364
R;Bevan, M.; Pohl, T.; Melranegger, T.; Bancroft, T.; Mewes, H.N.; Rudd, S.; Lemcke, A;Reference number: 124492
A;Reference number: 124492
A;Accession: 748364
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A;Molecule type: DAA
A;Molecule type: DAA
A;Rosaidess: 1-598 CMIL-
A;Crosa-references: EMBL:258319; PIDN:CAA92699.1; GSPDB:GN00020; CESP:723G7.1
A;Bxperimental source: clone T23G7
                                                                                                                                                                                                                                                          UP-2 transcription factor-like - Arabidopsis thaliana
N;Alternate names: protein 712911.60
C;Species: Arabidopsis thaliana (mouse-max cress)
C;Dete: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: 748768
R;Bayan, M.; #ilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.;
submitted to the Protein Sequence Database, April 2000
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A:Accession: 725207
                        A; Map position: 5
A; Introns: 36/2; !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :Molecule type: DNA
Residues: 1-413 (BEV)
|Cross-references: EMBL/AL162731
|EMBL/AL162731 | BAC clone F17E4
                                                                                         .9Seatus: preliminary
.HOlacule type: DNA
.Residues: 1-289 <BEV>
.Cross-references: EMBL:AL162971
.Experimental source: cultivar Columbia: BAC clone 722P11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 81.2%;
Best Local Similarity 83.3%;
Matches 30; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                 Reference number: 224490
Accession: 748268
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                   57/1; 71/3; 95/3; 142/3; 169/3; 198/3; 222/2
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Pred. No. 3.2e-13;
7; Mismatches 2; Indels
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equal
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hypothetical protein 124020.40 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 22-Oct-1999
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C;Species: Caenorhabditis elegans
C;bate: 39-Oct.1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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A;Experimental source: clone Y48CJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Regiduss: 1-470 <MIL>
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submitted to the EMBL Data Library, September 1999
A; Reference number: Z21046
A; Accession: T31602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                  A; Introns: 12/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the Protein St
A: Reference number: 117586
A:Accession: T13005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: $2/3; 156/2; 206/2; 237/3; 332/1; 386/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: CESP:Y48C3A.t
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MAC
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Best Local Similarity
Matches 25; Conserv
Query Match
Best Local Similarity
Matches 15; Conserv
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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75.64;
                                         38.7%;
4; Mismatches
                                         Score 72; DB 2;
Pred. No. 0.03;
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Pred. No. 3
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    8
                                                                              Length 323;
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C; Species: Mus musculus (house mouse)

A56209

RESULT 11

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C;Date: 28-Apr-1995 #Bequeuro______C;Accession: A56209
C;Accession: A56209
R;Li, Y: Slansky, J.E.; Mysrs, D.J.; Drinkwater, N.R.; Kaelin, W.G.; Parnham, Nol. Cell. Biol. 14, 1861-1869, 1994
A;Title: Cloning, chromosoms1 location, and characterization of mouse E2F1.
A;Reference number: A56209; MUID:94158858
A;Accession: A56209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription factor E2P1 - human

**NALEARNAKE names: Ap12 protein; retinoblastoma-associated protein; retinoblastoma-bindi
C:Species: (name)
C:Date: 22-Oct-1996 *sequence_revision 01-Nov-1996 *text_change 02-Jun-2000
C:Accession: JC4929; A45032; A42998; A42997; I54091
R:Neuman, E; Sellers; W.R.; McNeil, J.A.; Lavrence, J.B.; Kaelin Jr., W.G.
Gene 173, 163-169, 1996
A:Title: Structure and partial genomic sequence of the human E2F1 gene
A; Accession: JC4929; MUID:97082961
A; Accession: JC4929
                                                 A; Molecule type: mRNA
A; Residues; 1-312; 5, 314-321, Mr. 323-328, T. 330-437 KARS
A; Cross-references: GB:UJ1851; NID:9555713
A; Cross-references: GB:UJ1851; NID:9555713
A; Experimental source: Akata cells; expression vector pGEN-27K
A; Mote: sequence extracted from NCB1 backbone (NCBIN:110018, NC
R; Johnson; D.G.; Ohtani, K.; Nevins, J.R.
Genes Dev. B. 1514-1525, 1994
                                                                                                                                                                                                                                                                                             A:Wolecule type: mRNA
A;Residues: 1-312,'S',314-321,'N',323-328,'7',330-437 <FEL>
A;Residues: 1-312,'S',314-321,'N',323-328,'7',330-437 <FEL>
A;Residues: 1-312,'S',314-321,'N',323-328,'7',330-437 <FEL>
A;Ross-references: GB:M96577; MTD:gl81917; PID:gl81918
A;Experimental source: Naim 6 pre-B laukemia cell line
A;Ross-reference extracted from NCBI backbone (NCBIN:110015, NCBIP:110016)
R;Roselin JT., WGs., Krek, N.; Sellers, N.R.; DeCaprio, J.A.; Ajchenbaum, P.; Fuchs, C
Cell 70, 353-364, 1992
Cell 70, 353-364, 1992
A;Ross-reference number: A42997; MUID:92346721
A;Ross-reference number: A42997; MUID:92346721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Holecule type: mRNA
A:Realduss: 'LCRORRPOAERDRALAEACRHGDAPPPPPPVTRAARAVSV', 1-312,'S',314-321,'N',323-328,'T',
A:Realduss: 'LCRORRPOAERDRALAEACRHGDAPPPPPPVTRAARAVSV', 1-312,'S',314-321,'N',323-328,'T',
A:ROCE: sequence extracted from NCBI backbone (NCBIE:119095)
A:NOCE: the authors are uncertain whether Het-1 is the initiator or whether translation
R:Hetlin K, Lees JA.; Vidal, M.; Dyson, N.; Harlow E.; Fattaey, A.
Cell 70, 337-350, 1992
A:Title: A cDNA encoding a pRB-binding protein with properties of the transcription fact
A:Reference number: A42998; MUID:93346720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: placenta R;Shan, B.; Zhu, X.; Chen, P.L.; Durfee, T.; Yang, Y.; Sharp, D.; Lee, W.H. R;Shan, B.; Zhu, X.; Chen, P.L.; Durfee, T.; Yang, Y.; Sharp, D.; Lee, W.H. Mol. Cell. Biol. 12, 5620-5631, 1992

A;Titla: Molecular cloning of cellular genes encoding retinoblastoma-associated A;Reference number: A45032; MUXD:93078763

A;Accession: A45032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Status: preliminary: nucleic acid sequence not shown
A:Holecule type: DMA
A:Residues: 1-137 (ARGU)
A:Ross-references: GB:U47675; NID:g1594281; GB:U47676; NID:g1594282; GB:U47677;
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Best Local Similarity 43.6
Matches 14; Conservative
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Residues: 1-430 <LIA>
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Ory control of E2F1 expression 154091; MUID:95047311
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Pred. No. 0.049;
B; Mismatches
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                                                         A; Map position: 1p36-1p36
C; Keywords: transcription
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A54595
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F; 118-190/Domain: F; 191-241/Region:
                                                                                                                                                                                                                                 A; Map position: 20q11-20q11
A; Introns: 87/3 118/1 191/2 242/2 280/3 355/1
C; Keywords: DNA binding: transcription factor
F; 67-108/Redion: cyclin box Factus predicted
F; 118-190/Domain: DNA binding status predicted
                                                                                                                                                                                                                                                                                                                                             A/Cross-references: GDB:134661; OMIM:189971
                                                                                                                                                                                                                                                                                                                                                               ;Accession: 154091
;Status: preliminary: translated from GB/ZMBL/Duby,
;Molecule type: DNA
;Residues: 1-88,'R','T',122-123,'TPR',127,'QRR',297-299,'PRR',308-309,'RA',312,'C'
;Residues: GB:S74230; MID:g712816; PIDM:AAD14150.1; PID:g4261850
                                                                                                                Dest Local Similarity 43.8%;
164 KRRIYDITNYLEGIQCIAKXSKNHIQMLGSHT 195
                                                4 RRRVYDALNYLMAMNIISKE-KKEIKWIGLPT 34
                                                                                               Conservative
                                                                                                                                                                                                             7-residue
                                                                                            8; Mismatches
                                                                                                                   Score 71.5; DB Pred. No. 0.05;
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                                                                                               9
                                                                                                                                          Length 437;
                                                                                               Indels
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R:Ivey-Hoyle, M.; Conroy, R.; Huber, H.E.; Goodhart, P.J.; Oliff, A.; Heimbrook, Mol. Cell. Biol. 13, 7802-7812, 1993
A;Title: Cloning and characterization of EZF-2, a novel protein with the blochemia; Reference number: A54595; MUID:94067141
A;Recession: A54595
A;Recus: preliminary
A;Holecule: type: mRNA
A;Residues: 1-437 <IVE> A:Status: preliminary A:Holecule type: mRNA A:Residues: 1-403 <PAS> R;Pastenu, S.; Loisesu, L.; Arnaud, L.; Trembleau, A.; Brun, G. submitted to the EMRL Data Library, June 1993
A;Description: Isolation and characterization of a chicken homolog A;Reference number: \$58345
A;Accession: \$58345 A;Cross references: GDB:270248; OMIM:600426 A;Hap position: 1p36-1p36 transcription factor E2F-2 - buman C:Species: Homo sapiens (man mil) C:Date: 13-73n-1955 #sequence\_revision 13-Jan-1995 #text\_change 08-Oct-1999 C:Accession: A54599 A;Residues: 1-403 <PAS>
A;Cross-references: EMBL:x89245; NID:g944827; PID:g944828 A;Gene: GDB:E2F2; E2F-2 A;Cross-references: GB:L22846; NID:g410206; PIDN:AAA16890.1; PID:g410207 Query Match 37.9
Best Local Similarity 44.8
Matches 13; Conservative ]?-1 transcription factor - chicken |Species: Gallus gellus (chicken) |Date: 14-Jan-1996 #Bequence\_revision 01-War-1996 #text\_change 10-Sep-1997 141 KRRIYDITNYCEGIQLITKKSKNNIQWLG 169 \* RRRYYDALNVLMAMNIISKE-KKEIKWIG 31 37.9%; Score 70.5; DB 2; Length 403; Pred. No. 0.063; B; Mismatches 7; Indels protein with the blochemics 1 of the E2P-1 tre ۳

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-805 cONTY
A;Residues: 1-805 cONTY
A;Residues: 1-805 cONTY
A;Cross-references: GB:U10184; NID:g499103; PIDN:AAA19003.1; PID:g499104
A;Cross-references: GB:U10184; NID:g499103; PIDN:AAA19003.1; PID:g499104
R;Dynlacht, B.D.; Brook, A.; Dembski, M.; Yenush, L.; Dyson, N.
Proc. Natl. Acad. Sci. U.S.A. 91, 6359-6363, 1994
A;Title: DNA-binding and trans-activation properties of Drosophila E2F and DP proteins.
A;Reference number: A55745; MUID:94294381
A;Accession: A55745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcription factor E2F-1 - fruit fly (Drosophi, melanogaster)
G;Species: Drosophila melanogaster
G;Date: 28-Apr-1995 sequence_revision 28-Apr-1995 stext_change 21-Jul-2000
G;Accession: A56199; A55745
R;Ohtani, K.; Nevins, J.R.
Mol. Cell. Biol. 14, 1603-1612, 1994
Mol. Cell. Biol. 14, 1603-1612, 1994
A;Title: Functional properties of a Drosophila homolog of the E2F1 gene.
A;Reference number: A56199; MUID:94158833
A;Accession: A56199
                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Genetics:
A;Gene: FlyBase:E2fl
A;Cross-references: FlyBase:FBgn0011767
   Search completed: August 28, 2002, 12:59:59 Job time: 130 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.SCatus: preliminary: nucleic acid sequence not shown
A.SCatus: preliminary: nucleic acid sequence not shown
A.Residues: 1-805 cDYN>
A.Cross-references: GB:X78421; NID:g515868; PIDN:CAA55186.1; PID:g516869
                                                                                                                                                                                                                                                                                   Query Match 36.3%; Score 67.5; DB 2; Length 805; Best Local Similarity 48.1%; Pred. No. 0.36; Matches 13; Conservative 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 37.41; Score 69.5; DB 2; Length 437; Best Local Similarity 44.81; Pred. No. 0.095; Matches 13; Conservative 7; Mismatches 8; Indels 1
                                                                                                                                                      7: Indels 1; Gaps
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Run on:
                                                                                                              OM protein - protein search, using aw model
August 28, 2002, 12:55:14; Search time 29.9 Seconds (without alignments)
137.449 Million cell updates/sec
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Title: Perfect score: US-09-900-147-1 186

Sequence: 1 ENIBERTYDALNYLMAMNIISKEKKEIKWIGLPTNSA 37

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5 747574 segs, 111073796 remidues

Total number of hits satisfying chosen parameters:

747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match (%)
Maximum Match 100%
Listing first 45 summaries

Database : A\_Geneseq\_032802:

1: /SIDSI/gcgdata/hold-geneseq/geneseqp-cmbl/AA1980 DA7:

2: /SIDSI/gcgdata/hold-geneseq/geneseqp-cmbl/AA1981 DA7:

3: /SIDSI/gcgdata/hold-geneseq/geneseqp-cmbl/AA1981 DA7:

4: /SIDSI/gcgdata/hold-geneseq/geneseqp-cmbl/AA1981 DA7:

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9: /SIDSI/gcgdata/hold-geneseq/geneseqp-cmbl/AA1981 DA7:

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21: /SIDSI/gcgdata/hold-geneseq/geneseqp-cmbl/AA1996 DA7:

22: /SIDSI/gcgdata/hold-geneseq/geneseqp-cmbl/AA1996 DA7:

23: /SIDSI/gcgdata/hold-geneseq/geneseqp-cmbl/AA1996 DA7:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by enalysis of the total score distribution.

## SUDDIARIES

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11	- นผม - มหต เ- ต ณ	Result
153	200000	Score
84.9 82.3	100.0 100.0 100.0 100.0 100.0 100.0 89.8 89.2	Query
120	200044 20004 20004 20004 20004	Length
222	222222222	BG
AAB33108 AAB33007	AAM30501 ABG05510 AAG74072 AAAR54663 AAAR89313 AAAR89313 ABG28057 AAX18026 ABB60853 ABG05508	Ħ
Pinus radiata tran Pinus radiata tran	OP-1 transcription Novel human diagno Human colon cancer Transcription fact Transcription fact Novel human diagno Novel human diagno Novel human diagno	Description

Human transcription DP-1 transcription Novel human diagno	16 AAR71734 19 AAW30511 22 ABG01756	165	37.4 36.8	69.5	222
E3P1 transcription Human transcription Retinoblastoms pro		437 437	38. 8.	777	555
Transcription fact Homo sapiens E2F1		437	38.4	71.5	38
Mutant E2F1 transc		196	38.4 38.4	71.5 71.5	38
E2P activity inhib		15	38.7	72	<b>3</b>
E2F·like transcription		281	39.0	72.5	= =
E29-		272	40.1	74.5	ភ
DP-1	19 AAW30516	1 2		7 <b>7</b>	55
p-1		19	12.5	79	6
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E2F activity i	19 33457051	28		55	: =
DP-1 transcription		20	54.3	101	üï
Amino acid sequenc	22 AAB67762	192	51.5	133	; <u>:</u>
Pragment		56	71.5	133	ö
Impatiens		138	73.1	136	Ó
Corn DP-2	20 ANY32164	194	77.4		œ <b>`</b>
Arabidopsis		344	9 69 1 . 22	151	3 0
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Arabidopsis chalis		277	81.2	151	•
DP-l'transcription	EMAS	30	81.7	152	w
Caenorhabditis ele	20 AAW83389	575	B2	153	5

## **ALIGNMENTS**

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AAW30501 standard; Peptide; 37

AAW30501;

26-OCT-1998 (first entry)

DP-1 transcription factor paptide H (DEP box).

DP-1; transcription factor; antagonist; E2P protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy.

Synthetic. Homo sepiens.

WO9828334-A1.

02-JUL-1998.

22-DEC-1997; 97WO-GB03506

20-DEC-1996; 96GB-0026589.

(PROL-) PROLIFIX LTD.

WPI: 1998-377596/32.

Bandara LR, La Thangue NB;

Polypeptide fragments of the DP-1 transcription factor  $\cdot$  used for inducing apoptosis, specifically in tumour and cardiovascular cells. e.g. for preventing restanosis

Claim 1; Page

44; SSpp; English

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Peptide # (I) comprises residues 163-199, i.e. the DEF box region, confirmance plated fragents (II) (see AN#30502-07) cc of (I) are capable of antagonising the heterodiments action of a DP cc of (I) are capable of antagonising the heterodiments action of a DP cc of (II) comprising (I) or (II) and a membrane translocation sequence (III) comprising (I) or (II) and a membrane translocation sequence (C (I)-(III) are used therspeatically to induce apoptosis, comprising the perfect of the particular calls, either in vivo or in (I)-(III) are used the repeatically to induce apoptosis, comprising complete the particular calls, either in vivo or in (I)-(III) are used to treat or prevent restensis in patients who have undergone angioplasty, (I)-(III) function by inactivating comprising companies and applicably. (I)-(III) function by inactivating comprising companies of DP/E2F heterodimers. They are also used as research reagents, as positive controls in assays for identifying antagonists of DP-/Z2P dimerisation and as immunoassay contents action and as immunoassay agents. Also described is the use of sequences antisense to specific acids encoding (I)-(III) to control DP levels in cells particularly by gene thereby. When formulated with cytotoxic cor cytostatic agents, (I)-(III) enhance call killing.
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Best Local S
Matches 37
New isolated polynucleotide and encoded polypaptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                               Drmanac RT.
                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG05510;
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                                                                                                                                                                  N-PSDB; AAS69697.
                                                                                                                                                                                                NPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #5501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-PEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                             (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 100.0%; Score 186; DB 19;
Local Similarity 100.0%; Pred, No. 9.8e-22;
hes 37; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                             HYSEO INC.
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                                                                                                                                                                                                                                                           Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein: 149
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invention relates to

isolated polynucleotide (I) and

AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer essociated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene

Claim 20; SEQ ID No 35869; 103pp; English.

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CC polypeptide (II) sequences. (I) is useful as hybridisation probes, complymerase chain rescrion (PCR) primers, ollipomars, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, datecting or QII), (II) is useful for generating antibodies against it, datecting or CC quantitating a polypeptide in tissue, as molecular velyht markers and as a food supplement. (II) and its binding partners are useful in medical CC inaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrent protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC anino acid sequences. ABGIO010-ABGIO077 represent novel human CC those the sequence data for this patent did not appear in the printed case policitication, but was obtained in electronic format directly from HIPO case for the sequence data for this patent did not appear in the printed case policitication, but was obtained in electronic format directly from HIPO case for the sequence as a content of the sequence of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 37; Conservative 0
                                                                                                                                                                                                                            WPI; 2001-235357/24.
N-PSDB; AAH33503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinome; chromosome 13.
                                                                                                                  Claim 11;
                                                                                                                                                         Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                             Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                        29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-2000; 2000WO-US26524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human colon cancer antigen protein SEQ ID NO:4836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG74072 standard; Protein; 355 AA.
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                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENONE SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200122920-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                             Page 6620-6621; 9803pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                     9905-0157637.
9905-0163780.
                                                                                                                                                                                                                                                                                                Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0) Mismatches
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Pred. No. 5.3e-21;
), Mismatches 0;
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RESULT
AARS4663
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Best Local Similarity 100.0%;
Matches 37; Conservative 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR54663;
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                                                             DNA encoding novel transcription factor DP-1 was obtained from F9-EC cells. The DNA can be used to produce recombinant DP-1, or in gene therapy as a means of treating the uncontrolled proliferation of a.g. tumor cells.
                                                                                                                                                                                                                                           Novel transcription factor DP-1 and its recombinant production . for diagnosis end treatment of diseases associated with abnormal ETF or ETF-1 and family expression, esp. proliferative diseases
                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-167464/20.
N-PSDB; AAQ65344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-1992;
05-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus sp.
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N.B. Pages 666 to 682 and page 7053 of the sequence listing were
missing at time of publication, meaning no sequences are present for
SBQ ID ND:1037 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                        LA THANGUE NB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-1993;
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           Sequence
                                                                                                                                                                                               Disclosure: Page 49-50; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MEDI-) MEDICAL
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93GB-0016206.
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Pred. No. 1.5e-20;
Ni. Mismatches 0;
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Query Match 100. Best Local Similarity 100. Matches 37; Conservative

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Score 186; DB 17; Pred. No. 1.8e-20; Mismatches 0;

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Best Local Similarity
Matches 37; Conserv
                   DP-1 (AARB9212) is part of the DP-1/E2P-1 transcription factor complax. It is phosphogylated during the cell cycle, and has a greater affinity for night when in a hypophosphorylated state. This finding can be used to assay for agents which prevent or inhibit DP-1 hypophosphorylation or which enhance the phosphorylation of DP proteins. Such agents can be used to prevent or dalay entry of the cell cycle into 5 phase from G1 useful in traking proliferative diseases. Antibodies against regions of DP-1 which undergo changes in phosphorylation (see AAR89213) can also be used in such assays, and identify proliferating cells.
                                                                                                                                                                            Assays for potential growth prevention, inhibiting or enhancing agents - eap. DP protein phosphorylation modulation agents, used to provent or delay entry of cell into S phase from G, useful in treating proliferative diseases
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                                                                                                                                                                                                                                            NPI; 1996-087752/09.
N-PSDB; AAT10582.
                                                                                                                                                                                                                                                                                                                                                      03-JUL-1995;
                                                                                                                                                         Claim 6: Page 38-40; 54pp; English.
                                                                                                                                                                                                                                                                                                                                01-JUL-1994;
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phosphorylation; cell proliferation; therapy; diagnosis.
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ilarity 100.0%;
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Pred. No. 1.8e-20;
Nismatches 0;
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ggkkkidkgkkeefekkuknonnonnonnonnonnonnon
                                                                                                                                                                                                                                        CC The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences: (I) is useful as hybridisation probes, CC polyperase chain reaction (PCR) primars, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II) The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping activity of (II) or to treat disease states involving CC (II). (II) is useful in gene therapy tachniques CC (II). (II) is useful in gene therapy tachniques CC (II). (II) is useful in gene therapy tachniques CC (II). (II) and its binding partners are useful in medical CC (II). (II) and its binding partners are useful in medical CC (Insigned a stressing (II). (I) and (II) are useful for treating CC (Insigned a stressing (II). (I) and (II) are useful for treating CC (Insigned a not polynucleotide sequences have applications in CC (Insigned and polynucleotide sequences have applications in CC (Insigned and polynucleotide sequences have applications in CC (Insigned and product dependent on DNA and CC (Insigned and cold sequences of the invention).

CC (Insigned and polynucleotide sequences of the invention) but was obtained in electronic format directly from WIPO at fire the printed cold acquence of the sequences.
                                                                                               Query Match
Best Local Similarity
Matches 37; Conserv
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                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 58416; 103pp; English.
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N-PSDB; AAS92244.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #28048.
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(HYSE-) HYSEQ INC.
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                                                                                                                                                                                                              424 AA:
                                                                                       llarity 100.0%; (Conservative 0;
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                                                                                          Score 186, DB 22,
Pred. No. 1.9e-20;
); Mismatches 0;
                                                                                                                                      Length 424;
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26-MAR-2002 (first entry)

ABB60852;

ABB60852 standard; Protein; 445

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RESULT
NAY18026
ID ANY1
                                                                                                                                                                                                                                                                                                                                 This sequence is the murine DP-Jalpha isoform.

CC The invention relates to the DP-Interacting protein (DIP), that contains the Invention relates to the DP-Interacting protein (DIP), that contains the BIP-POP. domain, and is a potent transcriptional repressor that can call and immunogen or to raise antibodies. Such antibodies are useful in the purification and disgnostic screening methods. DIP polypeptides may be used to screen for modulate its activity. Such molecules used to serve for molecules which modulate its activity. Such molecules are useful in therapeutic contexts, e.g. in connection with conditions to the involve abnormal or abstrant expression of DIP. Modulators of DIP CC which involve abnormal or abstrant expression of DIP. Modulators of DIP CC which involve abnormal or abstrant expression of DIP. Modulators of DIP CC such as seminomas and teratomas, and in the promotion of melosis. DIP CC such as seminomas and teratomas, so probes and primers, and for conditions associates of alleles, mutants, variants and conditions associated with disorders of germ calls, including transfer such as deminomas and teratomas.
                                                                                                                        Query Match 97.8%;
Best Local Similarity 97.3%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIP: DP-interacting protein; BTB/POZ domain; transcriptional repressor; DP-dependent transcription; immunogen; cycle control; seminome; teratome diagnosis; meiosis promoter; proliferative disorder; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY18026 standard; Protein; 446
Dischosure; Page 73-76; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DP transcription factor-interacting protein designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-347716/29.
N-PSDB; AAX76730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De La Luna S, La Thangue NB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNIU ) UNIV GLASCOW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ж09927091-Л1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine DP-3alpha isoform protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-1999
                                                                                                                                                                                                                                                                                   116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97GB-0024828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98NO-GB03485.
                                                                                                                                                    Score 182; DB 20;
Pred. No. 8.4e-20;
                                                                                                                        1; Mismatches
                                                                                                                               0
                                                                                                                                                                                    Length 446;
                                                                                                                               Indels
                                                                                                                           0
                                                                                                                           Caps
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Query Match 89.2%;
Best Local Similarity 86.1%;
Natches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleir acid detection reagent capable of detecting 1000 or more games from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutich drugs. The invention discloses genomic DNA sequences (ABL16176 ABL16176 ABL16175) and the encoded proteins (ABB73737-ABB73072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
30-MAR-2001; 2001WO-US08631.
                                                       11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 9348; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI: 2001-656860/75.
N-PSDB; ABL04955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000U8-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W0200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 9348.
                                                                                                      W0200175067 - A2.
                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                  Novel human diagnostic protein #5499.
                                                                                                                                                                                                                                                                                                                    13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      ABG05508 standard; Protein; 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'ama 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 166; DB 22;
Pred. No. 2.6e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myer8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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RESULT 10
ABB33108
ID ABB3311
XX ABB3311
XX 25-JAN
XX 25-JAN
XX Plant:
XX Plant
XX V90000
XX W02000
XX W02000

NO200053724 - A2 Pinus radiaca. Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogang; bilp; G-box binding factor; basic halix-loop-helix zipper; homeotic; homeodomain; homeobox; WADS; homeodomain zipper; LIM domain; AP3; EREBs; zinc linger domain; type 2 Cys3His3; CCANT box element; MYB.

Pinus radiata transcription factor protein sequence #235.

25-JAN-2001 (first entry)

AAB33108;

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Conservative

Indels

0 S PS

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AAB33108 standard; Profitin; 119 AA

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The invention relates to isolated polynucleotide (I) and CC polyseptide (II) sequences. (I) is useful as hybridisation probes, polyseptide (II) sequences. (I) is useful as hybridisation probes, polyseptide (II) reaction (PCB) primers, oligomers, and for chromosome CC polyserse chapting and in recombinant production of (II). The contifying expressed sense (I) is useful in gene therapy techniques (C polynucleotides are also used in disgnostics as expressed sequence tags (II). (II) as useful in gene therapy techniques (II). (II) is useful in gene therapy techniques (II). (II) as useful in gene therapy techniques (II). (II) as useful in gene therapy techniques (II). (II) and its binding partners are useful in medical cannot properties expressing (II). (I) and (II) are useful in medical cannot properties and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have application of materiary consisting for enseting the consisting the consisting sequences and polynucleotide sequences have application DNA and CC and ocid sequences as segions to bloodies other types of data and products dependent on DNA and CC shots: The sequences assignment of the invention.

Consisting the consisting patent of the invention of the sequence of the invention towal human conditional conditions of the invention.

Conditionally the sequence of the invention of the printed conditions of the invention of the printed conditions of the invention.

Conditionally the printed in electronic format directly from wiponic at fig. viponic polynublished pot_sequences.
  Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID No 35867; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT, Llu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
23-AUG-2000;
                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-639362/73.
DB; AAS69695.
                                                                                                                                 185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0540217.
2000US-0649167.
                          87.11;
89.21;
Score 162; DB 22;
Pred. No. 3.8e-17;
2; Mismatches 2;
                                                   Length 185;
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RESULT 11
AAB3300
ID AAB330
AXX
XX
AAB330
AXX
XX
XX
XX
ZS-JAN
XX
DE Pinus
XX
CP Pinus
XX
C
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Best Local Similarity 86.1
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiate. The present sequence is one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a plant having motified gene expression such as a woody plant e.g. a cucalyptus, pine, ocacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polyperide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: b2IP, b2IP family of G-box binding factors, basic helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain ilper, lim domain, AP2 and BREBS, zinc finger domains of type 2 Cys2His2, CCAAT box elements and MYB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant: transcription factor; gene expression; eucalyptus; pine; acacla; popilar; sweetgum; tesk; mahogan; blie; G-box binding factor; basic helix-loop-helix ripper; homeotic; homeodomain; homeobox; WADS; homeodomain ripper; LIN domain; AP2; EREBs; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB.
                                                                                                                        11.WAR-1999;
18-AUG-1999;
                                                                                                                                                                                                                                            09-MAR-2000; 2000WO-US06112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pinus radiata transcription factor protein sequence #134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB33007 standard; Protein; 120
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(GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD
                                                                                                                                                                                                                                                                                                                            14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                    WO200053724-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pinus radiata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 - MAR - 1999;
18 - AUG - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-NAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 AA;
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                                                                                                                   99US-0266513.
99US-0149485.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>..</u>
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Pred. No. 9.4e-17;
3; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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RESULT 12
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Best Local S
Matches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel plant transcription factors from Eucalyptus grandle or Pinus radiata. The present sequence is one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a sucalyptus, pine, acacis, poplar, sweetgum, teak, or mabogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, besic helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain in the proper is the domain, AP2 and EREBS, zinc finger domains of type 2 cys2His2, CCAAT box elements and MYB.
                                     Novel LIN-37, -35, -55, -52, -53 and -54 gene from C. elegans - usaful for treating diseases associated with altered levels of cell proliferation, e.g. carcinomas
                                                                                                                                           109
                                                                                                                                                                                                                                                                                                                                        LIN-55; synthetic multivulva; SynMuv; signal transduction; animal model; tumour suppressor; retinoblastoma; cancer; cancer; cell proliferation; gene therapy.
                                                                                               WPI, 1999-045352/04.
N-PSDB: AAV72852.
                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans synNuv protein LIN-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW83389 standard; Protein; 575 AA.
                                                                                                                                                                                                   28-MAY-1997;
                                                                                                                                                                                                                               28-MAY-1998;
                                                                                                                                                                                                                                                            03-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
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                                                                                                                                                                                                                                                                                      MO9854299-A1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 390; 747pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-579369/54.
                                                                                                                                                                      (NASI ) NASSACHUSETTS INST TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C, HOTVILZ HR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 AA;
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                                                                                                                                                                                                  9705-0047996.
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Pred. No. 5.7e-16;
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Claim 7; Fig 8; 70pp; English

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RESULT 13
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Best Local Similarity 75.7%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DP-1; transcription factor; antagonist; E2F protein; cell proliferation; cardiovascular cell; restenosis; surgical stent; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DP-1 transcription factor antagonist peptide H7
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WPI; 1998-377596/32.
                                                                                                                                                                                                                                                                    21-DEC-1997;
                                                                                                                                                                                                                                                                                                                                         02-JUL-1998.
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                                                                 Bandera LR,
                                                                                                                                                                                                                                                                                                                                                                                                              W09828334-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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                                                                                                                                                                                               96GB-0026589.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "Claim 3"
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Pred. No. 3.8e-15;
7; Mismatches 2;
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Peptide H7 comprises smino acid residues 170-199 in the DEF box (II) (see AAN930501) of transcription factor DP1. Claimed peptides (II) (see AAN93050-07) containing one or both of 2 motife (see AAN930502-03) of the DEF box are capable of sntagonising the haterodimerisation of a by protein with an ZEP protein. Also claimed are verifants of these peptides, especially containing substitutions of residues corresponding to residues 167, 159, 171 and 175 of DP-1, fusion proteins (II) comprising (I) or (II) and a membrane translocation sequence (see AAN9308), expression vectors encoding (I)-(III) and host cells. (I)-(III) are used to rerapeutically to induce apoptosis, specifically in tumour or cardiovascular cells, either in vivo or in vitro, e.g. for purging bone marrow. Surgical stents comprising (I)-(III) are used to treat or prevent restencis in patients in hot have undergone ansionly (I)-(III) function by inactivating the DMA-binding are suppliesty. (I)-(III) function by inactivating the DMA-binding ansignists of DP-1/ZIP heterodimers. They are also used as research reagents, as positive controls in assays for identifying antagonists of DP-1/ZIP dimerisation and as immunoassay agents. Also described is the use of sequences entisense to nucleic acids encoding (I)-(III) to control DP laves in cells, particularly by gene therapy. When formulated with cycotoxic or cytostatic agents, and cell is shance cell killing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 44; SSpp; English.
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용 ð Query Match 81.7%; Score 152; DB 19; Best Local Similarity 100.0%; Pred. No. 1.5e-16; Matches 30; Conservative 0; Mismatches 0; Length 30; Indels 0 Caps .

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AAG22852
TO THE REPORT OF THE PROPERTY 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2000 (first entry)
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Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tunour and cardiovascular cells,

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Best Local Similarity 83.3%;
Matches 30; Conservative
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25-0(7-1999)
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21-0C7-1
Transgenic plants comprising an expression cassette consisting of a DP nucleic acid, when expressed, the nucleic acid increases the efficiency of plant cell transformation by increasing the number of dividing cells in the plant.
                                                                                                                                                                                                                                                               W0200047614 - A1.
                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                    tea mays.
                                                                                                                                                                                                                                                                                                                                                                             DP polypeptide: transcription factor; gene transcription; cell cycle; DNA replication; DRTF; differentiation-regulated transcription factor 1; transgenic plant; transformation efficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                     A corn transcription factor designated DP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB07975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB07975 standard; Protein; 299
                                                                        WPI; 2000-524530/47.
N-PSDB; AAA59702.
                                                                                                                                                                                                   11-PEB-2000; 2000WO-US03651.
                                                                                                                                                                                                                                  17 - AUG - 2000 .
                                                                                                                                            (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                           12-PEB-1999:
                                                                                                                 Love KS, Gordon-kamm NJ, Bailey MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9909-0119857.
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9908-0161104
9908-0161105
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9908-0161151
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9908-01611993
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                         /note- "any amino acid encoded by NNN"
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3-0160770.
3-0160814.
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                                                                                                                 Gregory CA;
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Disclosure: Page 71-72: 76pp; English.

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                                         The present sequence represents a corn DP (not defined) polypeptide. The polypeptide is a transcription factor that activates transcription of numerous genes involved in DNA replication, thus playing a role in the G1 to S transition in the cell cycle. Do, also called DRTP (differentiation-regulated transcription factor 1) has been shown to form specific multiprotein complexes with the retinohastoms susceptibility protein, pl07, cyclins and cdkl. The DP polynucleotide proteins are useful for increasing transformation efficiency in plants by increasing the number of dividing cells in the plant (dividing cells may be more receptive to transformation).
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Sequence 299 AA;

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Query.Match 81.2%;
Best Local Similarity 83.3%;
Matches 30; Conservative
Score 151; DB 21;
Pred. No. 3.5e-15;
3; Mismatches 3;
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Search completed: August 28, 2002, 12:59:14 Job time: 240 sec

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# Copyright (c) 1993 - 2000 Compugen Ltd.

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Total number of hits satisfying chosen parameters: Minimum DB seq length: 0
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Database :

Sw188Prot\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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P58105 P5	014186 008639 014318 022703 022703 022703 04917 054917 054917 04009 01094 001094 001094 001091 001091 001091 001091 001091	Description
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25.3	25.3	25.3	25.3	25.3	25.5	25.5	25.5	25,5	25.5	25.5	25.0
556	556	556	263	258	4568	2032	1435	615	594	259	1928
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TCPA_CRIGR	TCP2_MOUSE	TCP1_HOUSE	CLPE_ECOLI	FAER_ECOLI	DYHC_CAREL	CTOG_HUMAN	LTE1_YEAST	SPPA_HAZIN	T410_ARATH	PSA3_CAEEL	MYS1_YEAST
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## ALIGNMENTS

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Matches 37
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SEQUENCE
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-I- HISCELLANGOUS: E2P/DP TRANSACTIVATION CAN BE MEDIATED BY SEVERAL -
-- COPACTORS INCLUDING TBP, TFIIH, MDM2 AND CBP.

-I- SINILARITY: BELONGS TO THE E2P/DP FAMILY.
                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDILING-93188967: PubMed-8446173;
Girling R., Partridge J.F.,
Girling R., Partridge J.F.,
Hsuan J.J., la Thangue N.B.;
*A new component of the transcription factor DRTP1/E2F.*;
Nature 362:83-87(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L23959; AAA58440.1; ...
HSSP: Q14188; ICE7.
INTER 18902: ...
InterPro; IPR003316; E2F_TDP.
Pfam; PF02319; E2F_TDP; I.
Transcription regulation; DNA-binding; Activator; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWALS Institute of Bioinformatics and the ENGL outration the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no vay modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license(18b-sib.ch).
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NIVAOO
NIVAOO
DEVELOPMENTAL EXPRESSION. MEDITINE-98025478; PubMed-9376316;
                            Girling R.;
Summitted (JUL-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                    Nus musculus (Mouse).
Eukaryota; Metazoa; C
Nammalis; Eutheria; F
                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Transcription factor DP-1 (R2P dimerization partner 1) (DRTF1-
                                                            REVISIONS TO C-TERMINAL.
                                                                                                                                                                           NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                  163
                                                                                                                                                                                                                                                                                                                                                                            BRAIN, PLACENTA, LIVER AND KIDNEY. LOWER LEVELS IN LUNG PANCREAS. HOT DETECTED IN HEART. INDUCTION: DOWN-REGULATED DURING DIFFERENTIATION. PHOSPHORYLATION BY E3F-1-BOUND CYCLIN A-CDK2, IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195
                                                                                                                                                                                    Chordata;
Rodentla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45070 MH;
                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 186; DB 1; 100.0%; Pred. No. 9.2e-19; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
DEF BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENHANCES BINDING OF RB PROTEIN TO E2F.
POLY-PRO.
ASP/GLU-RICH (ACIDIC) (NCB DOWAIN).
PBOSPHORYLATION (BY CDKZ) (POTENTIAL).
3FEEFELE49FD9EDO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIMERICATION (PCTENTIAL)
DCB1.
                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                              410 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 410;
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45230

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CC PUNCTION: CAN STRUILATE EST-EDEPHNOEMT TRANSCRIPTION. BINDS DAN COOPERATIVELY WITH ESP PANILY MEMBERS THROUGH THE 22 RECOGNITION CC SITE, TTTCC/GCGC, POUND IN THE PROMOTER REGION OP A MUMBER OP GENES WHOSE PRODUCTS ARE INVOLVED IN CELL CYCLE REGULATION OF GENES WHOSE PRODUCTS ARE INVOLVED IN CELL CYCLE REGULATION OF IN DIA REPLICATION. THE 6P2/22F COMPLEX FUNCTIONS IN THE COMPLEX COMPONENT OF THE DYSTIF SET OF COMPLEX COMPLEX COMPONENT OF THE DYSTIF SET OF COMPLEX CAN EXPERD FROM CL TO S PHASE. THE ESP-IND COMPLEX CAN EXPERD FROM COMPONENT OF THE DYSTIF SET OF COMPLEX CAN INTERACT WITH HYPOPHOSPHORYLATED RETINOBLASTOMA PROTEIN REI AND COMPONENT OF THE DYSTIF SET OF COMPLEX CAN INTERACT WITH HYPOPHOSPHORYLATED RETINOBLASTOMA PROTEIN REI AND COMPONENT OF THE COMPONENT OF THAN EXPERSE OF TRANSCRIPTIONALLY ACTIVE. VIRAL CHESTORY WITH DATA COMPONENT OF TRANSCRIPTIONALLY ACTIVE. VIRAL CHESTORY WORLD WAS RELEASING THE ACTIVE COMPLEX.

CC PRESENTIATED AND MESSENTHALL EPITHELLUM, FIRST EXPRESSED OF SEQUESTERING ARE PROTEIN, THE INTERTINAL TISSUES, LEVELS IN CREASING BY SUPELIABLE CONTINUES.

CC PRESENTIATION AT 15 5 DPC, DP-1 EXPRESSION INCREASES IN THE INTERVILLUS EPITHELLAL COMPARMENT. WITH EXTRELION WITH LOWER LEVELS IN THE INTERVILLUS EPITHELLAL COMPARMENT. WITH EXPELS IN THE INTERVILLUS EPITHELLAL COMPARMENT. WITH EXPELS IN THE INTERVILLUS EPITHELLAL COMPARMENT. WITH EXPELS IN THE EXPELS IN THE EXPELS FROM 11.5 AND 13.5 DPC IN THE EXPRESSION INCREASES IN THE EXPELIPM PROBLEM OF THE MESSENT FAIL SET OF THE VERTIFICATION OF THE THYROS. ALSO POWED AT LOWER LEVELS IN THE DEVELOPING RETINAL BURNES, EXPRESSED NOTH IN TERTINOBLAST AND COMPRESSED IN SECRETAL WISCOMEN LAYERS STATED. WEART AND CHONDROTTES. WEAKLY EXPRESSED OF THE MESSENT FOR COMPARSE TOWN CHORDED PLEWED.

CC PRESENT IN KILDREY, LUNE, LIVER, HEART AND CHONDROTTES. WEAKLY EXPRESSED OF THE CHORDROTTES. THE COMPAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: X72310; CAA51056.1;
HSSP; Q14188; 1CP7.
HGD; HGT:101934; Tfdp1.
InterPro; IPR003316; E2P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *Expression patterns of the E2F family of transcription factors during murine epithelial development.*;
Cell Growth Differ. 8:533-563(1997)
-1- FUNCTION: CAN STINULATE E2F-DEPENDENT TRANSCRIPTION. BINDS DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97294022; PubMed-9149906; Dagnino L., Fry C.J., Bartley S.M., Phillips R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Expression patterns of the E2F family of transcription factors during mouse nervous system development.", wech. bev. 66:13-23(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR003316; E2F_TOP:
Pfam: PP02319; E2F_TOP: 1.
Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL EXPRESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed-9149906;
                                                                                                                                                                                                                                                                                                                                                                                    cycle.
DIMERIZATION (POTENTIAL).
DCB1.
DCB1.
DCB2.
DCB2.
POLY-PRO.
ASP/GLU-RICH (ACIDIC) (NCB DCMAIN).
PHOSPHONYLAVION (BY CDM2) (POTENTIAL).
PM : PERAO9OC78107189 CRC64;
                                                                                                                                                                                                                                                                                                          DEF
                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear protein;
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8

Query Match 100 Best Local Similarity 100 Matches 37; Conservative

100.01; <u>.</u>

Score 186; DB 1; Pred. No. 9.2e-19; ; Mismatches 0;

Length 410;

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0 Caps

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A PART CRESTALLOGRAPHY (2.6 ANGSTROMS) OF 121-215.

RY NERGY CRESTALLOGRAPHY (2.6 ANGSTROMS) OF 121-215.

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RY TERROCTION: FRANCE OF DAY TEOGRAPH THE PROPERTY OF TH
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Q1418B; Q14187; Q13331;

F 15-7UL-1999 (Rel. 39, Last sequence update)
F 30-MAY-2000 (Rel. 39, Last sequence update)
F 16-OCT-2001 (Rel. 40, Last annotation update)
F 18-OCT-2001 (Rel. 40, Last annotation update)
F 7848C-1915ton factor DP-2 (E2F dimerization partner 2).
F 1808C-2015ton factor DP-2 (E2F dimerization partner 2).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-WEARTINCEYERS;
TISSUE-96353862; PubMed-8755520;
MEDLINE-96353862; PubMed-8755520;
Rogers K.T., Higgins P.D.R., Mills M.M., Phillips R.S., Horowitz J.M.;
Rogers K.T., Higgins P.D.R., Mills M.M., Phillips R.S., Horowitz J.M.;
PP-2, a heterodimentic partner of E2F; identification and Characterization of DP-2 paroteins expressed in Mills Vo.*;
Proc. Matl. Acad. Sci. U.S.A. 93:7594-7599(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-102 FROM W.A. (ALPHA ISOFORM).

Thang Y., Chelluppen S.P.,

"Transcriptional activation and expression of DP transcription
factors during cell cycle and TPA-induced U937 differentiation.
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-95303470; PUDMAG-7784053; Thang Y., Chellappan S.P.; *Cloning and characterization of human partner of E2P.; *Oncogene 1077005-2093(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (DELTA ISOPORM), AND CHARACTERIZATION. MEDILINE-95257935; Pubhaed-7739537; MI C.L., Sukerberg L.R., Myvu C., Harlow E., Lees J.A.; "In vivo association of E2F and DP family proteins."; Nol. Cell. Biol. 15:2536-2546(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 62-79 FROM N.A. (DELTA ISOFORM),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A. (DELTA ISOFORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DP2, a novel dimerization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ONA
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Best Local S
Matches 37
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DROME

Similarity 37; Conserv

100.0%; ilarity 100.0%; Conservative 0

<u>..</u>

Score 186; DB 1; Pred. No. le-18; ; Mismatches 0;

Length 446; Indels

<u>.</u>

6

TDP\_DRONE STANDARD; 024318, 15-7UL-1998 (Rel. 36, Crested) 15-7UL-1998 (Rel. 36, Last seq 15-DEC-1998 (Rel. 37, Last sna

Transcription

factor dp.

annotation

update) on update)

PRT;

377 ζ

Drosophila melanogaster (Pruit fly).

Euksryota; Mecazos; Arthropoda; Trachesta; Hexapoda; Insupersysota; Meoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila.

NCBL\_TexID-7237;

[1]

Muscomorpha;

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EMBL: U.40386; AAA69016.1; -.
EMBL: U.5488; AAB60378.1; -.
EMBL: U.5488; AAB7321.1; -.
EMBL: U.5117; AAC50642.1; -.
PDB: 1CF7; 02-APR-99.
TRANSFAC: T03000; -.
                                                                                                                                                                             Phosphorylation; ONA_BIND 129
DOMAIN 176
DOMAIN 219
DOMAIN .229
                          VARSPLIC
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bidinformatics and the EMB outstation - the European Bidinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensessab-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>; ;</del>
                                                                                                                                                                                                                                                   InterPro: IPR003316; B2F_TDP.
Pfam, PF02319; E2F_TDP; 1.
Transcription regulation; DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÷
SEQUENCE
                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                 MIM; 602160;
                                                                                                    VARSPLIC
                                                                                                                       for Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDDUESTERING RB PROTEIN, THUS RELEASING THE ACTIVE COMPLEX.
SUBCELLULAR LOCATION: NUCLEAR
ALTERNATIVE PRODUCTS: AT LEAST 4 ISOPORMS; ALPHA/49 KDA (SHOWN HERE), BETA/43 KDA, GAMMA AND DELTA/48 KDA; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: HIGH LEYELS IN HEART AND SKELETAL MUSCLE. ALSO FOUND IN PLACENTA, KIDNEY, BRAIN, LUNG AND LIVER. THE PRESENCE AS MELL AS THE ABUNDANCE OF THE DIFFERENT TRANSCRIPTS APPEAR TO VARY SIGNIFICANTLY IN DIFFERENT TISSUES AND CELL LINES.
PTN: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE E2F/DP FAMILY.
18 2
                             64
                                                                        103
                             173
                                                                                               440100
                                                                811
49236 MH;
                                                                                                                                                                                                                                     cycles
                        DIMERIZATION (POTENTIAL).

DCB1.

DCB1.

DCB2.

ASP/GLU-RICH (ACIDIC) (NCB DOMAIN).

PHOSPHORYLATION (BY CDK2) (POTENTIAL).

PHOSPHORYLATION (BY CDK2) (POTENTIAL).

PHOSPHORYLATION (BY CDK2) (POTENTIAL).

MISSING (IN ISOFORM BETA, ISOFORM GAMMA AND ISOFORM DELTA).

MISSING (IN ISOFORM BETA AND ISOFORM GAMMA).

S -> SG (IN ISOFORM GAMMA).
                                                                                                                                                                                                        DNA-binding: Activator: Nuclear protain;
le: Alearnative splicing: 3D-structure.
POTENTIAL.
DEF BOX.
/FTId=VAR_002272.
19A6C85BAD61DFF1 CRC64;
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TDPH_CAREL SIRVE TOPH_CAREL SIRVE (22703)

7 15-JUL-1990 (Rel. 36, Created)

7 10-MAY-2000 (Rel. 39, Last sequence update)

7 30-MAY-2000 (Rel. 39, Last annotation update)

7 30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 89.7
Best Local Similarity 86.1
Natches 31: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl.
-1- FUNCTION-1- SUBUNIT
                                                                                                                PlyBase: FBgn0011763; Dp.
Interpro: IPR003116; E2F TDP.
Pfam; PF021319; E2F TDP; I
Transcription regulation; DNA-binding; Nuclear protein.
DOMAIN
81 88 POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metaroa; Nematu
Rhabditidae; Peloderinae;
MCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94294381; PubMed-8022787;
Dynlacht 8., Brook A., Dembski M., Tenush
"DN-blading and trans-activation properti
                                                                                                                                                                                                                    REVISIONS.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM M.A.
STRAIN-BRISTOL NZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X79708; CAA56147.2; ALT_INIT.
H93P; Q14188; ICP7.
                                                                                                                                                                                                                                                                         Submitted (DEC-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. Natl Acad. Sci. U.S.A. 91:6359-5363(1994).

FUNCTION: CAN STIMULATE EXP-DEPENDENT TRANSCRIPTION.
SUBUNIT: HETERODINER OF ZF AND DP. COOPERATE TO GIVE SEQUENCE-
SPECIFIC DNA BINDING AND OPTIMAL TRANS-ACTIVATION,
SUBCELULAR LOCATION: Nuclear (Potential).
SIMILARITY: BELONGS TO THE E3F/DP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 AA;
                                                                                                                                                                                                                                                                                                                                                                       ans.
Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disk;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42683 MW; 868F180D242C3DDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.14;
                                                                                                                                                                                                                                                                           the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 166; DB 1;
Pred. No. 5.6e-16;
4; Mismatches, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of Drosophila E2F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>..</u>
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                                                                                                                                                                                          RETISSUE-SEASON N.A., AND ALTERNATIVE SPLICING.

RETISSUE-SEASON, and Kidney;

RY TISSUE-SEASON, and Kidney;

RY MEDLINE-SGO3891; PUNNED-SOURCE

RY MEDLINE-SGO3891; PUNNED-SOURCE

RY A new member of the DP family, DP-J, with distinct protein products

RY A new member of the DP family, DP-J, with distinct protein products

RY A new member of the DP family, DP-J, with distinct protein products

RY SUSPENSES B regulatory role for alternative splicing in the cell cycle

RY transcription factor DRTP1/C2P, ";

RO COCCUTE CAN STUDILATE E2P-DEPENDENT TRANSCRIPTION. BINDS DNA

CC SITE, TTTC./GCCC. DOUD, IN THE DREADERS TRANSCRIPTION OR IN

CC SITE, TTTC./GCCC. DOUD, IN THE DREADERS TRANSCRIPTION OR IN

CC CELL-CYCLE PROGRESSION FROM G1 TO S PHASE. THE E3P-1/DP CONFEX

CC CELL-CYCLE PROGRESSION FROM G1 TO S PHASE. THE E3P-1/DP COMPLEX

CC CELL-CYCLE PROGRESSION FROM G1 TO S PHASE. THE E3P-1/DP COMPLEX

CC CELL-CYCLE PROGRESSION FROM G1 TO S PHASE. THE E3P-1/DP COMPLEX

CC CELL-CYCLE PROGRESSION FROM G1 TO S PHASE. THE E3P-1/DP COMPLEX

CC CELL-CYCLE PROGRESSION FROM G1 TO S PHASE. THE COMPLEX CAN

CC CELL-CYCLE PROGRESSION FROM G1 TO S PHASE. THE E3P-1/DP COMPLEX

CC CELL-CYCLE PROGRESSION FROM G1 TO S PHASE. THE COMPLEX CAN

CC CELL-CYCLE PROGRESSION FROM G1 TO S PHASE. THE COMPLEX CAN

CC CELL-CYCLE PROGRESSION FROM G1 TO S PHASE. THE COMPLEX CAN

CC PONS HETERODILERS WITH E2P FAMILY MEMBERS, DETACHES FROM THE

CC PREFILES IN MOTABLY E1A, T-ANTIGEN AND HPV E7, ARE CAPABLE OF

CC DREFILES IN SPLEEN AND HEART.

CC PRINCES SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED. HIGHEST

CC PHASE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED. HIGHEST

CC INHIBITS E2P-MEDIATED DNA BINDING AND TRANSCRIVATION.

CC INHIBITS E3P-MEDIATED DNA BINDING AND TRANSCRIVATION.
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Best Local
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15-JUL-1998
30-NAY-2000
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30-MAY-2000 (Rel. 39, Last sequence update)
16-027-2001 (Rel. 40, Last amnotation update)
Transcription factor DP-2 (E2F dimerisation pt
TFDP2 OR DP2.
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Pfam; PF02319; EZF_TDP; 1;
Hypothetical protein; Transcription regulation; DNA-binding;
Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENBL: 168319; CAA92699.1;
HSSP: Q14188; 1CE7.
WormPep: 723G7.1; CE03702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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Rodentia;
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75.7%;
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; Pred. No. 6.3e
7; Hismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrate; Euteleostomi: Sciurognathi; Muridae; Muridae; Muridae; Muridae; Muridae; Musidae; Musidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT
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ere and employed

SOPPRESENTATIONS

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Query Match 53. Best Local Similarity 67. Matches 23: Conservative
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054917;
30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
16-OCT-2001 (Rel.
                                                                MEDILINE-98065940: PubMed-9403682;

MOTRE! M., Wenkel J., Bannister A.J., Kouzarides T., Hagemeist C.;

*An E2P-11ke repressor of transcription.";

*An E2P-11ke repressor of transcription.";

*An E2P-11ke repressor of transcription. BINDS DNA.

*COOPERATIVELY WITH DP PROTEINS THROUGH THE E2 RECOGNITION SITE.

*TTCC/GCGC. HAS A PREFERNCE FOR THE TTTCCGC E2P RECOGNITION SITE.

*TTCC/GCGC. HAS A PREFERNCE FOR THE TTTCCGC E2P RECOGNITION SITE.

*TTCC/GCGC. HAS A PREFERNCE FOR THE TTTCCGC E2P RECOGNITION SITE.

*GOULATE A SUBSET OF E2P-DEPENDENT GENES WHOSE PRODUCTS ARE

**AN EXPLANATION.** DETAILS NOT THE CYCLE BUT NOT FOR MORMAL CELL.

**CYCLE PROGRESSION.** OVEREXPRESSION DELAYS THE EXIT OF CELLS FROM

**THE S-PHASE (BY SIMILARTY).

**ISUBURIT: COMPONENT OF THE DETAILS MEMBERS.

**ISUBURIT: COMPONENT OF THE DETAILS MEMBERS.

**ISUBURIT: COMPONENT OF THE DETAILS MEMBERS.

**ISUBLICIAR LOCATION: Nuclear (Probable).

**ISUBLICIAR LOCATION: Nuclear (Probable).

**ISUBLICIAR LOCATION: Nuclear (Probable).
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SEQUENCE
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DOMAIN
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MOD_RES
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outsteation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPR003316; E2F_TDP:
Pfom; PF02319; E2F_TDP: 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; $79780; AAB35506
HSSP; Q14188; 1CP7,
HSGD; MGI:107167; Tfdp2
InterPro; IPR003316; E;
                                                                                                                                                                                                                                  An E2P
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DNA_BIND 129
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                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 ictivity protein)
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                                                                                                                                                                                                                                                                                                                                                                                    musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                              Rel. 39. Created)
Rel. 39. Last sequence update)
Rel. 40. Last annotation update)
[actor E2F6 (E2F~6) (E2F~binding site modulating
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PHOSPHORYLATION (BY C
PHOSPHORYLATION (BY C
MISSYMC (IN ISOPORM B
AND ISOPORM DELTA),
MISSING (IN ISOPORM B
GANNA),
S -> SQ (IN ISOPORM G
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POTENTIAL.
DRY BOX.
DIMBRITATION (POTENTI)
DCB1.
DCB1.
ASP/GLU-RICH (RCIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 98.5; DB 1;
Pred. No. 2.3e-05;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                      Cranlata; Vertebrata; Euteleostomi;
Sciurognathi; Nuridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> SQ (IN ISOFORM GANNA).
0E6E87AE8B82KE8A CRC64;
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ATION (BY CDK2) (I
ATION (BY CDK2) (I
N ISOFORM BETA, II
DH DELTA),
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, ISOFORM GAMMA
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SULT 8

PS_HUMAN STANDARD; PRT; 
C 075461:060544;
C 075461:000 (Rel. 39, Created)
T 30-MAY 2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
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Best Local S
Matches 15
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Homo sapiens (Human).
Eukaryota; Matazoa; Ch
Mammalls; Eutherla; Pr
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PP02319;
Transcription r
Cell cycle.
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DONAIN
DONAIN
DONAIN
"Z2F-6, a member of the E2P family that can behave as a transcriptional repressor.";
Proc. Natl. Acad. Sci. U.S.A. 95.2859-2895(1998).
-I- FUNCTION: INHIBITOR OF E2F-DEPENDENT TRANSCRIPTION. BINDS DNA COOPERATIVELY WITH DP PROTEINS THROUGH THE E2 RECOGNITION SITE TITTCC/GCCC. HAS A PREFERENCE FOR THE TITTCC/GCC LIKE RECOGNITION SITE SITE. E2F-6 LACKS THE TRANSCRIPTIONAL ACTIVATION AND POCKET PROTEIN BINDING DOMAINS. APPEARS TO REGULATE A SUBSET OF E2F-DEPRIDENT GREES WHOSE PRODUCTS ARE REQUIRED FOR ENTRY INTO THE CELL CYCLE BUT NOT FOR MORMAL CELL CYCLE PROGRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

HEDLINE-935613; PubMed-9689056;

GAUBALE S., MOOD J.G., Livingston D.M.;

"Unusual proliferation arrest and transcriptional

"Unusual proliferation arrest family member, E2F-6.";

proc. Natl. Acad. Sci. U.S.A. 95:9190-9195(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF032131; AAC53521.1;
HSSP; 016254; 1CF7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://vvv.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                  MEDIJINE-98368625; PubMed-9704927; Carteright P., Mueller #: Wagener #E2P-6; a novel member##f the E2P f dependent transcription, "; Oncogene 17:611-623(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro: IPR003316; E2F_TDP.
Pfam; PP02319; E2F_TDP; 1.
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NGD; MGI:1354159; E266.
                                                                                                                                                                                                      TISSUE-Fetal brain;
MEDLINE-98169460; PubMed-9501179;
Trimarchi J.M., Pairchild B., Verona
                                                                                                                                                                                                                                                                                              Oncogene
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-98368625;
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15; Conservative
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173
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POTENTIAL.
DEF BOX.
DIMERIZATION (POTENTIAL).
LEUCINE-TIPPER.
TRANSCRIPTION REPRESSION DOMAIN
(BY SIMILARITY ).
(BY SIMILARITY CRESSION CONTAIN
(BY CF42553DEADBBBBB CRC64;
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                                                                                                                                                                                                          R., Moberg K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                        R., Helin K.,
an inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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Query Match
Best Local Similarity 48.3
Conservative
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EMBL; AF061381; AAC14694.1; ...
HSSP; Q16254; ICF7.
MIM; 602944; ...
InterPro; IPR003316; E2F_TDP.
Pfam; PF03319; E2F_TDP; 1.
                                                                                                                                                                                  EZPL_MOUSE 210-2012 (Feb. 35, Created) 01:001; (Rel. 35, Created) 01:007-1997 (Rel. 35, Last sequence update) 10:MAY-2000 (Rel. 39, Last annotation update) 20:MAY-2000 (Rel. 39, Last annotation update)
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                             (1)
SEQUENCE FROM N.A.
STRAIN-SWISS ALBINO;
MEDIINE-54119858; Pubmed-8114719;
Plannky J.E., Myers D.J.,
                                                                                                                                                                                                                                                                                        BSDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation; DNA-binding; Repressor; Nuclear protein; Cell cycle.
DEVELOPMENTAL EXPRESSION.
MEDILINE-98025478; PubMed-9376316;
Dagnino L., Fry C.J., Bartley S.M., Farnham P., Gallie B.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIVAC
                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                            faraham P.J.;
                                                                                                                                                CBI_TaxID-10090
                                                                                                                                                                                                                                                                                                                                        100 KRRYDITHYLDGIDLYZKKSKNHIRWIG 128
                                                  loning, c
                                                                                                                                                                                                                                                                                                                                                      OVEREXPRESSION DELAYS THE EXIT OF CELLS FROM THE S-PHASE.
SUBURIT: COMPONENT OF THE DRTF1/E2F TRANSCRIPTION FACTOR COMPLEX.
FORMS HETERODINERS WITH DP FAMILY MEXBERS.
SUBCELLULAR LOCATION: Nuclear.
SUBCELLULAR LOCATION: Nuclear.
T15SUE SPECIFICITY: EXPRESSED IN ALL T15SUES EXAMINED. HIGHEST
LEVELS IN PLACENTA, SKELETAL MUSCLE, HEART, OVARY, KIDNEY, SMALL
INTESTINE AND SPLEEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE E2F/DP FAMILY.
                                                  chromosomal location, and characterization of mouse E2F1.^{+}, Biol. 14:1861-1869(1994).
                                                                                                                                                                                                                                                                                                                                                                                                 39.0%;
                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₹
                                                                                                                                                                                                                                                                                                                                                                                    Score 72.5; DB 1; Length 281; Pred. No. 0.0066; 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   I-YE: REDUCTION IN REPRESSOR ACTIVITY,
LITTLE EFFECT ON S-PHASE ENTRY.
AR -> HE (IN REF. 3).
I -> V (IN REF. 3).
G -> E (IN REF. 3).
539E049C15AD3508 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSCRIPTION REPRESSION DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIMERIZATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEF BOX.
                                                                                      Drinkwater N.R., Kaelin W.G.,
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                                        Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license(sb-sib.ch).
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FROM HETERODIMENS WITH DP PARTILLY MEMBERS. THE ESP-1 COMPLEX SPECIFICALLY HYPOPHOSPHORYLATED RETINOBLASTOMA PROTEIN RB1. DURING THE CELL CYCLE, RB1 BECOMES PROSPHORYLATED IN MID-TO-LATE G.

PHASE, DEFALUSES FROM THE DATFI/ESP COMPLEX, RENDERING ESP-1 COMPLEX SPECIFICALLY HYPOPHOSPHORYLATED RETINOBLASTOMA PROTEIN RB1. DURING THE CELL CYCLE, RB1 BECOMES PHOSPHORYLATED IN MID-TO-LATE G.

PHASE, DEFALUSES FROM THE DATFI/ESP COMPLEX, RENDERING ESP.

INTERSITING THE ACTIVE. ONMPLEX.

INTERSITING THE ACTIVE COMPLEX.

INTERSITING THE ACTIVE. ONMPLEX.

RELEASING THE ACTIVE. THE BRAIN, WITH HIGHEST LEVELS IN THE DEFELOPMENTAL STAGE: IN THE BEVELOPING HERVOUS SYSTEM, ENDERING ESPINAL CORD. EXPRESSION RESTRICTED TO THE HALL. B. DEFELOPMENTAL STAGE: IN THE BEATIN, FEARS AT DAY 13.5 AND DECLINES SPINAL CORD. FROM DAY 12.5, EXPRESSION RESTRACTED TO THE WENTAL THE DEVELOPING RETINA, EXPRESSION ESPINAL CORD FROM DAY 12.5, EXPRESSION IN THE DEVELOPING SPINAL CORD FROM DAY 13.5, EXPRESSION IN THE BEATINA, EXPRESSION IN CORD FROM DAY 13.5 AND DECLINES OFFICE OF THE BEATING RETINA, EXPRESSION IN LUKE. IN COMPLEX, LAYER. IN COMPLEX, LAYER. IN COMPLEX, EXPT. 15 EXPRESSION IN LIVER. LAYER. IN COMPLEX, EXPT. SHALL CARD. FROM DAY LAYER. SHALL CARD. FROM DAY LAYER.
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HOlnberg C., Helin K., Sehested M., Kerletroem O.;
"EZF-1-induced p53-independent apoptosis in transgenic mice.";
Oncogene 17:143-155(1998).
-1- FUNCTION: TRANSCRIPTION ACTIVATOR THAT BINDS DNA COOPERATIVELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: L21973; AAA83217.1; -...
HSSP: Q16254; 1CF7.
TRANSPAC: T00219; -...
TRANSPAC: T01543; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:101941; E2f1.
InterPro; IPRODJ316; E2;
Pfam; PF02319; E2F_TDP;
Transcription regulation
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SEQUENCE
430
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10316; EZE_TDP.
10316; EZE_TDP:
22F_TDP: 1.
2
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169
189
279
430
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                                                                                                              LEUCINE-EIPPER.

DEP BOX.

DIMERIATION (POTENTIAL).

TRANSACTIVATION (POTENTIAL).

RETINOBLASTONA PROTEIN RB1 BINDING
CSDE18AD3B4DFEFA CRC64;
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RESULT 10
E2F1_HUWAN STANDARD;
ID E2F1_HUWAN STANDARD;
AC Q01094; Q92768; Q13143;
DT 01-JUL-1993 (Rel. 26, Cre-
DT 01-JUL-1993 (Rel. 26, Les
Deloukas P., Hatthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
Jones H., Stavrides G., Almeida J.P., Babbege A.K., Baggulay C.L.,
RA Belley J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Bessley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W., Butler A.P., Cerder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.M., Clark S.Y., Clee C.M.,
RA Chapman J.C., Cobby V.E., Collier R.E., Connor F., Corby N.R.,
RA Chapman A., Crille G.J., Deadman R., Dhami F., Dunn M.,
RA Collson A., Crille G.J., Deadman R., Dhami F., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Hubble B., Hunt A.R., Hunt J.E., Jekosch K., Johnson C.M., Johnson D.,
RA Hambond S., Bairley J.L., Mesch P.D., Ho S., Holden J.L., Howden P.J.,
RA Hubble B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., Ring A., Knights A., Larlor S.,
RA Lebveslaiho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Hubble S., Mastry D., Moconnachle L.J., NaCay K., Howards A.A.,
RAIN M. Narin S.L., McConnachle L.J., NaCay K., Howards A.A.,
RAIN M. Narin S.L., McConnachle L.J., NaCay K., Howards A.A.,
RAIN M. Narin S.L., McConnachle L.J., NaCay K., Howards A.A.,
RAIN M. Narin S.L., McConnachle L.J., NaCay K., Howards A.A.,
RAIN M. Narin S.L., McConnachle L.J., NaCay K., Howards A.A.,
RAIN M. Narin S.L., McConnachle L.J., NaCay K., Howards A.A.,
RAIN M. Narin S.L., McConnachle L.J., NaCay K., Howards A.A.,
RAIN M. Narin S.L., McConnachle L.J., NaCay K., Howards A.A.,
RAIN M. Narin S.L., McConnachle L.J., NaCay K., Howards A.A.,
RAIN M. Narin S.L., McConnachle L.J., NaCay K., Howards A.A.,
RAIN M. Narin S.L., McConnachle L.J., NaCay K., Howards A.A.,
RAIN M. Narin S.L., McConnachle L.J., Nach R., McConnachle L.J., Nach R., McConnachle R., Parker A., Parker A., Parker R., Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 43. 
Watches 14; Conservative
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Eukaryota; Metazos; C
Mambalia; Eutheria; P
MCBI_TaxID=9606;
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01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last amotation update)
01-MAR-2002 (Rel. 41, Last amotation update)
Transcription factor E2F1 (E2F-1) (Retinoblastoma binding protein 3)
(RBBP-3) (PRB-binding protein E2F-1) (PBR3) (Retinoblastoma associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEDLINE-93078763; PubMed-1448092; AEDLINE-93078763; PubMed-1448092; Shan B., Ehu X., Chen P.L., Durfee T., Yang Y., Sharp D., Lee W.H.; Shan B., Ehu X., Chen P.L., Durfee T., Yang Y., Sharp D., Lee W.H.; Shan B., Ehu X., Chen P.L., Durfee T., Yang Y., Sharp D., Lee W.H.; Shan B., Ehu X., Chen P.L., Durfee T., Yang Y., Sharp D., Lee W.H.; Shan B., Sharp D., Lee W.H.; Sharp D., Lee W.H.; Shan B., Sharp D., Lee W.H.; Sharp D., Lee W.H.; Shan B., Sharp D., Lee W.H.; Sharp D., Lee W.H.; Shan B., Sharp D., Lee W.H.; 
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HEDLINE-92146720; PubMed-1638634;

Helin K., Lees J.A., Vidal N., Dyson N.J., Harlow E., Fattaey

Helin K., Lees J.A., Vidal N., Dyson N.J., Harlow E., Fattaey

*A cDNA encoding a pRB-binding protein with properties of the

transcription factor E2F.*;

Cell 70:337-350(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM H.A.

HEDLINE-97082961; PubMed-8964493;

Neuman E., Sellers W.R.S., McNell J.A., Lavrence J.B.,

Kaplin W.G. Jr.;

*Structure and partial genomic sequence of the human E2F1
cene 1731163-169(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM M.A. MEDILINE-92346721; Pubmed-1638635; MEDILINE-92346721; Pubmed-1638635; Raelin M.G. Jr., Krak W., Sellers W.R., Decaprio Puchs C.S., Chittenden T., Li Y., Farnham P.J., B Fuchs C.S., Chittenden T., Li Y., Farnham P.J., B Livingston D.M., Flemington E.K.; Expression cloning of a cDNA encoding a retinobl protein with E2P-like properties."; Cell 70:351-364(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein 1) (RBAP-1).
E2F1 OR RBBP3.
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Primates;
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8; Mismatches
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Catarrhini; Hominidae;
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Blanar M.A.,
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; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene.";
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TRANSCTIVATION INHIBITION.

TO TRANSCTIVATION INHIBITION.

Y MEDLING-94019324, Pubmed-8413249;

X HEDLING-94019324, Pubmed-8413249;

X HEDLING-94019324, Pubmed-8413249;

X HELLING-94019324, Pubmed-8413249;

X HELLING-9401931.

Y "Inhibition of E2F-1 transactivation by direct binding of the retanoblastoma protesin.";

Y "Inhibition of E2F-1 transactivation by direct binding of the retanoblastoma protesin. THROUGHT THE PROPOSERY THROUGH THE PROCESSION OF A WINDER OF GENES WHOSE PRODUCTS ARE INVOLVED IN CELL CYCLE REQUILATION OR IN DNA REPLICATION. THE DROFFERSTIALLY READ PROTEIN, IN A CELL-CYCLE DEPENDENT MANNER. IT CAN MEDIATE BOTH COMPANY OF THE PROPOSERY OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phillimore B.J.C.T., Prathelingam S.R., Plumb R.W., Ramsby H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steverd C.A., Sulston J.B., Svann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Yaudin M., Hall M., Hallis J.M., Whitehead S.L., Whitchead S.L., Whitchead T., Williams L.W., Williams S.A., Williams L., Williams S.A., Williams J., Williams S.A., Williams J., Williams S.A., Williams J., Williams S.A., Williams J., Williams S.A., Rogers J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUNCTION IN APOPTOSIS. 44
MEDILINE 99234788; Pubmed 9170954;
Wh X., Levine A.J.;
Pp3 and E2P-1 cooperate to media.
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MEDLING-95059071; Pubmed-7969176;

Nu M., Shepard K.-A., Peng C.-Y., Yee A.S.,

"Cyclin A/CDR2 binds directly to EZF-1 and in

activity of EZF-1/DP-1 by phosphorylation.";

MOI. Cell. Biol. 14:8420-8431(1994).
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MEDLINE-95047332; PubMed-7958856;
Bynlacht B.D., Flores O., Lees J.A., Harlow E.;
"Differential regulation of E2F transactivation complexes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYCLIN A/CDK2 BINDING DOMAIN.

MEDLINE-94306513; PubMed-803308;

Krak W., Even M.S., Shirodkar S., Arany Z., Kaelin W.G. Jr.,

Krak W., Even M.S., Shirodkar S., Arany Z., Kaelin W.G. Jr.,

Livingaton D.M.;

"Neigative regulation of the growth-promoting transcription f
"Neigative regulation of the growth-promoting transcription f
E2F-1 by a stably bound cyclin A-dependent protein kinase.";

Cell 78:161-172(1994).
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Taya Y., Nishimura S., Okuyama A.,
"Phosphorylation of 837-1 by cyclin
Oncogene 10:229-236(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-111 PROM M.A.

MEDLINE-95047311; PubMed-7958836;

MEDLINE-95047311; PubMed-7958836;

JOHNSON D.G., Ohteni K., Nevins J.R.;

JOHNSON D.G., Ohteni K., Nevins J.R.;

Autoregulatory control of 8391 expression in response and negative regulators of call cycle progression.";

Genes Dev. 8:1514-1535(1994).
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Proc. Natl. Acad. Sci. U.S.A. 91:3602-3606(1994).
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MEDLINE-97342624; PubMed-919931;
Dynlacht B.D., Mobarg K., Lees J.A., Harlow
"Specific regulation of E2F family members b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-95140412;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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CELL PROLIFERATION AND P53-DEPENDENT APOPTOSIS.

- SUBUNIT: COMPONENT OF THE DRYFI/ESP TRANSCRIPTION PACTOR COMPLEX.

FORMS HETERODIMERS HITH DP FAMILY MEMBERS. THE ESF-1 COMPLEX BINDS

SPECIFICALLY HYPOPHOSPHORYLATED RETIMOBLASTOMA PROTEIN RB1. DURING

THE CELL CYCLE, RB1 BECOMES PHOSPHORYLATED IN MID-TO-LATE G1

PHASE, DETACHES FROM THE DRYFI/ESF COMPLÉX, RENDERING ESF

TRANSCRIPTIONALLY ACTIVE. VIRAL ONCOPROPEINS, NOTABLY ESA, T
ANTIGEN AND HPY E7, ARE CAPABLE OF SEQUESTERING RB PROTEIN, THUS

RELEASING THE ACTIVE COMPLEX.

--- SUBCELLULAR LOCATION: NUCLEBY.

--- SUBCELLULAR LOCATION: NUCLEBY.

--- SINILARITY: BELONGS TO THE ESE/DP PAMILY.

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RESULT 11
E2F1_CHICK
                                                                                                                                                                                                                                                                                           Query Match 38.4
Best Local Similarity 43.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license spreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                              CONFLICT
CONFLICT
CONFLICT
SEQUENCE
ESFI_CHICK STANDARD; PRT; 403 AA 595977; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 30-NAY-2000 (Rel. 39, Last annotation update) 7ranscription factor ESFI (ESF-1). ESFI. Callus gallus (Chicken).
                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                      4 RRRVYDALNYLMAMNIISKE-KREIKWIGLPT 34
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164 KRRIYDITNYLEGIQLIAKKSKNHIQWLGSHT 195
                                                                                                                                                                      38.44;
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                                                                                                                                                            Score 71.5; DB 1; Length 437; Prad. No. 0.015; 8; Mismatches 9; Indels
                                                                                                                                                                                                             Y-C: NO RÉTINOBLASTOMA PROTEIN BINDING.
KRRLÓLESSCPARCR -> RTPGTPRRORRUCP
PRAPORANC (IN REP. 6).
S -> Y (IN REP. 4).
T -> N (IN REP. 4).
T -> N (IN REP. 4).
1003B3F654F0C6GDP CRC64;
                                                                                                                                                                                                                                                                                     retinoblastoma protein rel binding (potential).
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RESULT 12
E2F2\_HUMAN
ID E2F2\_H
AC Q14209
DT Q1-NOV
DT Q1-NOV

STANDARD;

137

℥

014209; 01-NOV-1997 01-NOV-1997 01-NOV-1997

(Rel.

35, Created)
35, Last sequence update)
39, Last annotation update)

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PR TRANSFAC: TO2951:

PR TRANSFAC: TO2951:

PR InterPro; IPR003316; E2F_TDP.

PR Pfam: pP02319: E2F_TDP.

PR Pfam: pP02319: E2F_TDP.

PR Pfam: pP02319: E2F_TDP:

PAR: PP02319: E2F_TDP:

PR Pfam: pP02319: E2F_TDP:

PR Pfam: pP02310: E2F_TDP:

PD0MAIN 135 171 DEP BOX.

PD D0MAIN 135 171 DEP BOX.

PD D0MAIN 175 392 RETINOBLASTONA PROTEIN RB1 BINDING

PD D0MAIN 175 392 RETINOBLASTONA PROTEIN RB1 BINDING
                                                                                                          Query Natch
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -II- PURCIDAR TENDICALLY ATOURTY THAT BINDS DNA COOPERATIVELY
WITH DP PROTEINS THROUGH THE E2 RECOGNITION SITE, TTYCC/GGC,
WITH DP PROTEINS THROUGH THE E2 RECOGNITION SITE, TTYCC/GGC,
FOUND IN THE PROPOTER REGION OF A NUMBER OF GENES WHOSE PRODUCTS
ARE INVOLVED IN CELL CYCLE REGULATION OR IN DNA REPLICATION. THE
DRTEI/E2P COMPLEX FUNCTIONS IN THE CONTROL OF CELL-CYCLE
PROFESION PROH G1 TO S PHASE, E2P-1 BINDS PREFERENTALLY RB)
PROFEIN, IN A CELL-CYCLE DEPENDENT MANNER: IT CAN MEDIATE BOTH
PROTEIN, IN A CELL-CYCLE DEPENDENT APPROVISES (BY SIMILARITY).

FURLIFY: COMPLEX FUNCTION AND P53-DEPENDENT APPROVISES (BY SIMILARITY).

FORMS HETERODIMERS WITH DP FAMILY MEMBERS. THE 2P-1 COMPLEX BINDS
FORMS HETERODIMERS WITH DP FAMILY MEMBERS. THE 2P-1 COMPLEX BINDS
FORMS HETERODIMERS WITH DP FAMILY MEMBERS. THE 2P-1 COMPLEX BINDS
FORMS HETERODIMERS WITH DP FAMILY MEMBERS. THE 2P-1 COMPLEX BINDS
THE CELL CYCLE, RB1 BECOMES PROSPHORYLATED IN MID-TO-LATE G1
THE CELL CYCLE, RB1 BECOMES PROSPHORYLATED IN MID-TO-LATE G1
THANGE, DETACHES FROM THE DRTEI/E2P COMPLEX, RENDERING E2P
TRANSCRIPTIONALLY ACTIVE. VIRAL ONCOPROTEINS, MOTORBLY E1A, T
ANTIGEN AND HPY 2F, ARE CAPABLE OF SEQUESTERING RB PROTEIN, THUS
RELEASING THE ACTIVE COMPLEX.

-1. SUBCELLULAR LOCATION: NUCLEAR.

-1. SUBCELLULAR LOCATION: NUCLEAR.

-1. SUBCELLULAR LOCATION: NUCLEAR.

-1. SINGLARITY: BELONGS TO THE E2FOD FAMILY.
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Pastesu S., Loiseau L., Arnaud L., Trembleau A., Brun G.;
"Isolation and characterization of a chicken homolog of the E2F-1
transcription factor.";
Oncogene 11:1475-1486(1995).
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Archogauria; Aves; Meognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
NCBL_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensesisb-sib.ch).
4 RRRYYDALNYLMAMNIISKE-KKEIKWIG 31
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141 KRRIYDITNYLEGIQLITKKSKNNIQWLG 169
                                                                                                                                                                                                                                                 AA: 4359 MN;
                                                                                                                                          37.91;
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Pred. No. 0.01
8: Mismatches
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78SEA320537C33ED CRC64/
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:1 8d
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Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla, Eutheria; Primates; Catarrhini; Hominidae; Homo.

Transcription factor E2F2 (E2F-2).

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Query Match 37.4
Best Local Similarity 44.1
Matches 13; Conservative
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MEDLINE-94067141; PubMed-8246995;

TVEY-HOYLE M., CORTOY R., Huber H.E., Goodhart P.J., Oliff A.,

Heimbrook D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and characterization of E2P-2, a novel protein with the biochemical properties of transcription factor E2F."; mai. Cell. Biol. 13:7802-7812(1993).
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EMBL: AL021154: CAA15949.1; ...
HSSP: Q16254; ICF7.
TRANSFAC; T01544; ...
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                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            Transcription
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                                                                                                                                                                                                                                                                                                                                 Pro: IPR003316; E2F_TDP.

Pr02319; E3F_TDP; I.

cription regulation; Activator; DNA-binding; Nuclear protein; cription; Cell cycle.
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196
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196
196
363
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                     37.4%;
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Score 69.5; DB 1; Length 437; Pred. No. 0.028: 7; Mismatches 8; Indels
                                                                                                                                                                                    LEGGINE-ZIPPER.
DEF BOX,
DIMERIZATION (POTENTIAL).
TRANSACTIVATION (POTENTIAL).
POLY-PRO.
                                                                                                                  RETINOBLASTOMA PROTEIN ASSOCIATION (POTENTIAL). 60541F4235507305 CRC64;
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RESULT 13
RESULT 10
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Theression patterns of the E2F family of transcription factors of trapression patterns of the E2F family of transcription factors of the patterns of the E2F family of transcription factors of the figure of the patterns of the E2F family of transcription factors of the figure of the factor of the figure of the factor o
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STRAIN-SMISS ALBINO! TISSUE-Fibroblast;
STRAIN-SMISS ALBINO! TISSUE-Fibroblast;
MEDLINE-SMOS4478; PubMed-9376316;
Dagnino L., Fry C.J., Bartley S.M., Farnham P., Gallie B.L.,
Phillips R.A.;
"Expression petterns of the E2P family of transcription factors
during mouse nervous system development.";
Mech. Dev. 66:13-25(1997).
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Eukaryota: Metazoa: Chordata:
Mammalla; Eutherla; Rodehtla:
MCBI_TaxID~10090;
EMBL; AF015948; AAB71671.1;
HSSP; O16254; 1CF7.
TRANSFAC; T02947; ".
NGD; MGT:1096340; E213.
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15-JUL-1998
30-Max-2000
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on factor E3F3 (E3F-3) (Fragment).
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RA HOMITS N., Nagase T., Miyajima N., Sezuka T., Jamaka A., Seto S.,

Beki N., Kawarabayasi Y., Ishikawa K.*I., Tabuta S.;

RY "Prediction of the coding sequences of unidentified human genes. II.

RY The Coding sequences of 40 new genes (KIAAOO4: KIAAOO8) deduced by

RY The Coding sequences of 40 new genes (KIAAOO4: KIAAOO8) deduced by

RY The Coding sequences of 40 new genes (KIAAOO4: KIAAOO8) deduced by

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RY THORTON. TRANSCRIPTION ACTIVATOR THAT BIRDS DNA COOPERATIVELY

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COMPARESSION FROM G1 TO SENASE. E2F-3 BIRDS SPECIFICALLY TO

RRYTHOSELASTOMA PROPERT HE DRYTH/E2F TRANSCRIPTION FACTOR COMPLEX

BIRDS COOPERATIVELY WITH DP-1 TO E2F SITES. HITH

RETHOSELASTOMA PROPERT RB1 AND RELATED PROFEINS (SUCH AS P107)

THAT INNIBITY THE E2F TRANSCRIPTION GOODALM.

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-1- SUBCELLULAR LOCATION: Nuclear.
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000716; Q15000;
01 NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transcription fector E2F3 (E2F-3).
E2F3 OR KLAA0075.
E2F3 OR KLAA0075.
EARTHOUGH (Human).
EARTHOUGH SUCHERIA; Primates; Catarrhini; Homini HCB_TaxID-9506;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Dyson N., Helin K.;
The retinoblastoms protein binds to a family of E2F transcription
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Pfam; PF02319; E2F_TDP; 1.
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POTENTIAL.
LEUCINE-ZIPPER.
DEP BOX. ZIPPER.
DINERIZATION (POTENTIAL).
TRANSACTIVATION (POTENTIAL).
P130 PROTEIN ASSOCIATION (POTENTIAL).
P130 PROTEIN ASSOCIATION (POTENTIAL).
P130 PROTEIN ASSOCIATION (POTENTIAL).
P130 PROTEIN ASSOCIATION (POTENTIAL).
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Pred. No. 0.031;
9; Mismatches 7; Indels
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ARBELINE-99077992: PubMed-9858578; Sasaki T., Savado T., Tamaguchi M., Shinomiya T.; Specification of regions of DNA replication initiation embryogenesis in the 65-kilobase DNApolaiphs-dZZF locus melanogaster.*; Nol. Cell. Biol. 19:547-555(1999).
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(27386; 077035;
(27386; 077035;
01-WOY-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
Transcription factor E2f (dE2F).
E2F OR E2F1 OR C66376.
Drosophila melanogaster (Fruit fly).
Eukaryota; Hetazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Hetazoa; Arthropoda; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

MCBI_TaxiD=7227;
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MEDLINE-9415693; PubMed-9114699;
Ohtani K., Mevins J.R.;
Punctional properties of a Drosophila
Mol. Cell. Biol. 14:1603-1612(1994).
[3]
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TISSUS-Eye imaginal disk;
TISSUS-Eye imaginal disk;
MEDLINE-94794381; Pubmed-9022787;
MEDLINE-94794381; Pubmed-9022787;
Dynlacht B.D., Brook A., Dembaki M.,
Dynlacht B.D., Brook A., Dembaki M.,
TMN-bidding and trans-dirivation pro
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EMBL; D38550; BAA07553.1;
H55P; Q16254; LCF7.
MIN; 600427; -
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STRAIN-OREGON-R:
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DIMERIANTION (POTENTIAL).

TRANSACTIVATION (POTENTIAL).

RETINGBLASTONA PROTEIN ASSOCIATION
(POTENTIAL).

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POLY-ALA.
CYCLIN A/CDX2
POLY-GLY.
POTENTIAL.
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properties of Drosophila
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Adams M.D., Celniker S.E., Rolt R.A., Evans C.A., Gocayne J.D.,
Ananatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F.,
RA George R.A., Lavis S.E., Richards S., Anbburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Ihong O., Chen L.X.,
RA Bathorn R.C., Rogers Y.-H.C., Blass) R.G., Champe M., Pfelifer B.D.,
RA Bathorn R.C., Rogers Y.-H.C., Blass) R.G., Champe M., Pfelifer B.D.,
RA Bathorn R.C., Rogers Y.-H.C., Blass) R.G., Champe M., Pfelifer B.D.,
RA Bathorn R.C., Beau A., Barnari J., Bersktarogiu L., Beasiey E.M.,
RA Bathorn R.M., Basu A., Barnari J., Barnakari D., Bothakov S.,
RA Beson R.Y., Beancs P.V., Berman B.P., Bhandari D., Bothakov S.,
RA Berson R.Y., Beancs P.V., Berman B.P., Bhandari D., Bothakov S.,
RA Berson R.Y., Beancs P.V., Berman B.P., Bhandari D., Bothakov S.,
RA Berson R.Y., Beancs P.V., Berman B.P., Dhandari D., Bothakov S.,
RA Cherry J.M., Carley S., Dohlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dev I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dev I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dev I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dev I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dev I., Dietz S.M.,
RA de Pablos B., Coupt L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Herris H.L., Harvey D., Halsan T.J., Harnander J.R., Houck J.,
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RA Harris H.L., Harvey D., Halsan T.J., Harnander J.R., Houck J.,
RA Harris H.L., Harvey D., Halsan T.J., Harnander J.R., Houck J.,
RA Harris H.L., Harvey D., Halsan T.J., Holled H.H., Holke Y.,
RA Harris H.L., Harvey D., Halsan T.J., Holled H.H., Holke Y., Lin X.,
RA Harris H.M., Malsan F., Karpen G.H., Ka Z., Renison D.L.,
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STRAIN-BERKELEY;
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loterPro; IPR00316; E2F_TDP.
Pfam; PP02319; E2P_TDP: 1
TranscriptLon regulation; DNA-t
Developmental protein; Activate
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EMBL; UJ0184; AAA19003.1; --
EMBL; AB031813; BAA32766.1; --
EMBL; AE003735; AAF55904.1; --
HSSP; 016254; 1CF7.
TRANSFAC; T01547; --
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                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DIMERIZATION (POTENTIAL).
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POLY-ALA.
GLY-RICH.
POLY-SER.
POLY-RICH.
POLY-RICH.
POLY-GLY.
H -> Q (IM REF. 1 AND 2).
H -> Q (IM REF. 1 AND 2).
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Query Match 36.3%; Best Local Similarity 48.1%; Matches 13; Conservative 291 KRRIYDITHVLEGINICEKKSKNNIQW 317 4 RRRVYDALNYLMAMNIISKE-KKBIKW 29 Score 67.5; D Pred. No. 0.1; 6; Mismatches DB 1; Length 805; Indels ۲, GB PG ۳

28,

2002, 13:03:16

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Regult
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Meximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein search, using aw model
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Match
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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   11. Appl.
11. Appl.
11. Appl.
12. Appl.
13. Appl.
13. Appl.
14. Appl.
15. Appl.
16. Appl.
17. Appl.
18. Appl.
18. Appl.
18. Appl.
18. Appl.
18. Appl.
19. Ap
                                                                                                                                                                                                                                                                                                                                                                         RESULT 2 Claims ON AT US-08-428-131-11
GENERAL INFORMATION:

APPLICANT: La Thanque, Nicholas Barrie
TITLE OF INVENTION: Transcription Factor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS;
ADDRESSEE: Nixon 6 Yanderhye
STREET: 1100 NO. 5863757th Glebe Road, 8th Floor
CITY: Ariington
STATE: VIrginia
COUNTRY: U.S.A.
IIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 100.0%; Score 186; D84; Best Local Similarity 100.0%; Pred Mo 1.3e-21; Matches 0; Mismatches 0;
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35.2	35.2	37.1	37.4	37.4	38.4	38.4	38.4	38.4	38.4	36.4	38.4	38.4	38.4	38.4	38.4	38.4	40.9
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US-08-836-582-2	US-08-481-814A-8	11-566-80C-60-Sn	US-08-481-814A-7	US-08-136-119-2	PCT-0S93-11310-14	US-08-139-937-14	US-09-189-627A-13	US-08-801-092-1	US-08-462-174-3	US-08-481-814A-6	US-08-723-415B-13	US-07-882-711-2	US-08-136-119-4	US-08-481-814A-9	Š		US-09-308-935-5
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## ALIGNMENTS

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Sequence 1, Application US/09308939

Patent No. 6268334

GENERAL INFORMATION:

APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REPERRICE: 620-67

CURRENT APPLICATION NUMBER: 92/09/308/935

CURRENT FILING DATE: 1999-05-27

EARLIER APPLICATION NUMBER: PCT/GB97/03506

EARLIER APPLICATION NUMBER: DS 9636589.7

EARLIER APPLICATION NUMBER: GB 9636589.7

EARLIER APPLICATION NUMBER: GB 9636589.7

EARLIER APPLICATION NUMBER: SD 9636589.7

EARLIER FILING DATE: 1996-12-20

SOFTWARE: PATENTIAL DATE: 2.1
; TYPE: PRT
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-1
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US-09-308-935-1
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11, Application U8/08428131 5. 5863757

Length 37; Indela

0 Gaps

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/428,131
FILING DATE: 3-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ARTHUR R. CRAWFORD
REGISTRATION UNMBER: 15,37
REFERENCE/DOCKET NUMBER: 117-181
TELECOMMUNICATION INFORMATION:
TELEFAR: (703) 816-4100
TELEFAR: (703) 816-4100
                                                                                                                                                                                                                      CONFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-D05/MS-D05
SOPTMARE: Pacentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/05/078,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/428,131 FILING DATE: 23-JUN-1995 CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPUTER: IBM PC compatible PERATING SYSTEM: PC-DOS/MS-DOS PTWARE: Patentin Release #1.0, RENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JCANT: La Thangue, Nicholas Barrie
LE OP INVENTION: Transcription Factor DP-1
RR OF SEQUENCES: 14
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37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Release #1.0, Version #1.25 (EPO)
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 37; Conservative 0
                                                                   Ouery Match 100.0%; Score 186; DB 3; Best Local Similarity 100.0%; pred, No. 2.3e-20; Matches 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release (1.0)
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                  TELEPHONE: 703-815-4000
                                                                                                                                                                           COLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICARY: LaThangue, NICHOLAS B.

IPPLICARY: GOLAIUNG, SUSSAS

'ITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOPORMS

ITLE OF INVENTION: THEREOP
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KNIRRRYYDALNYLMANNIISKEKKEIRWIGLPTNSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-8EP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 KNIRRRYDALNYLMANIISKEKKEIKWIGLPTNSA 40
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5859199
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                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: NIXON & VANDERHYE P.C.
1100 NO. 5859199th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 186; DB 4
Pred. No. 3e-21;
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                                                                                                     Length 410;
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RESULT 9 19-08-723-415B-11 ; Sequence 11, Application US/08723415B

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; WOLECULE TYPE: protein US-08-723-4158-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 186; DB 2; Best Local Similarity 100.0%; Pred. No. 2.3e-20; Matches 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                       equence 2, Application US/08428131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                    STREET: LICE
CITY: Arlington
CITY: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC COMPUTENS
OPERATING SYSTEM: CC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MBER OF SEQUENCES: 21
JRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 410 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/01
FILING DATE: 30-3EP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Arlington
STATE: VA
                                                                                                                                                                                                                                   PLICANT: La Thengue, Nicholas Barrie
TLE OF INVENTION: Transcription Factor DP-1
MBER OF SEQUENCES: 14
RRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLICART: LaThangue, Nicholas B.
PLICART: deLaluna, Susana
TLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TLE OF INVENTION: THEREOF
APPLICATION DATA:
                                                                                                                                                                                             2: Nixon & Vanderhye
1100 No. 5863757th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB 9510195.1
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; MOLECULE TYPE: protein US-08-428-131-2
US-08-602-846-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 100.0%; Score 186; DB 2; Best Local Similarity 100.0%; Pred. No. 2.3e-20; Matches 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 816-410
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quence 2, Application US/08602846 cent No. 5871901
                                                                                                                                                                                                                                                                                                                                                           EIP: 22201-4714
COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMAT
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPELICAMT: Le Thangue, Nicholas B
NITLE OF INVENTION: ASSAT FOR INHIBITORS OF DP-1 AND OTHER DP
NITLE OF INVENTION: PROTEINS.
                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: mmino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DORESSEE:
                                          amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8th Ploor, 1100 No. 5871901th Glebe Road
                                                                                                                                                                                                                                                                                                           Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05/08/428,131
                                                                                                                                                                                                                                                                        US/08/603,846
                                                                                                                                                                     620-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Ouery Match: 100.0%; Score 188; DB 2; Length 410; Best Local Similarity 100.0%; Pred, No. 2.38-70; Natches 37; Conservative 0; Mismatches 0; Indele

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MOLECULE TYPE: protein US-09-078-596-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 100.0%; Score 186; DB 4; Length 410; Best Local Similarity 100.0%; Pred. No. 2.3e-246.
Natches 37; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09078596
Patent No. 6150116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                   CURRENT APPLICATION NUMBER: US/09/189,627A
CURRENT FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR PILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR FILING DATE: 1996-05-15
                                                                                                                                                                                                                                                                                                        09-189-627A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: U5/08,
FILING DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
HAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,3;
                                                                                                                                                                                                                                                       Tuence 10, Application US/09189627A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PAtentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,596
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Thangue, Nicholas Barrie
TITLE D'INVENTION: Transcription Pactor DP-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1100 No.
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDRESSEE:
                                                                                                                                                                                                                                           NEORMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EE: Nixon & Vanderhye
1100 No. 6150116th Glebe Road, 8th Floor
                                                                                                                                                                         La Thangue, Micholas
de la Luna, Susana
ERTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
                                                                                                                                                            620-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/428,131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
COMPUTER READABLE PORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 KNIRRRYDALNYLJAMNIISKERKEIKWIGLPINSA 199
                                                                                                                                                                                                                                                                                                             ITLE OF INVENTION: TRANSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KNIRRAYDALMYLMANNIISKEKKBIKWIGLPTHSA 37
                                                                                                                                                                              CITY: Arlington
STATE: VA
                                                                                                                                                                                                                                           DDRESSEE:
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Length 410; Indels

<u>..</u> Caps

pplication US/18723415B

1100 No. 5859199th Glebe Rd.

8th floor

TRANSCRIPTION PACTOR DP-3 AND ISOFORMS

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; TYPE: PRT
; ORGANISM: mouse
US-09-189-627A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 100.0%; Score 186; DB 4; Best Local Similarity 100.0%; Pred. No. 2.3e-20; Matches 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEO ID NO 10
                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/189,627A CURRENT FILING DATE: 1998-11-10 PRIOR APPLICATION NUMBER: 08/723,415 PRIOR FILING DAYE: 1996-09-30
                                                                                                                                                                                                                                                                                                                                          ·09-189-627A-11
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Lent No. 619691
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                                                                                                                                                                                                                                                   de la Luna
                                                                                                                                                                                                                                                                    La Thangue, Nicholas
                                                                                                                 1996-05-15
                                                                                                                                                                                                                                      TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 410;
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APPLICATION NUMBER: US/08/723,4158 FILING DATE: 30~SEP~1996

APPLICATION DATA:

GB 9610195.1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
NFORMATION FOR SEQ ID NO: 4: V

REPERENCE/DOCKET NUMBER: 11

SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

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) ORGANISM: mouse
US-09-189-627A-4
                                                                                                                                                                                                                  Query Match 97.8%;
Best Local Similarity 97.3%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: U5/09/189,627A
CURRENT FILING DATE: 1998-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 1996-
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICART: LATHANGUE, NICHOLAS B.
PPLICART: DELALUME, SUSANA
TYLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
ITLE OF INVENTION: THEREOF
                                                                                                                                                        APPLICATION NUMBER: GB o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4, Application US/09189627A
3. 6159691
                                                                                                                                                                                                                                                                                                                                                                         PatentIn Ver.
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de la Luna, Susana
                                                                                      pplication US/087234158
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milarity 97.3%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                              08/723,415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 182; DB 2: Length 369; Pred. No. 8.4e-20; Indels
                                                                                                                                                                                                                                 Score 182; DE 4; Length 369; Pred. No. 8.4e-20;
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Overy Match 97.8%, Score 182; D8 4; Length 370; Best LOCal Similarity 97.3%; Pred. No. 8.4e-20; Natches 35; Conservative 1; Mismatches 0; Indels

5

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GRGANISM: mouse
US-09-189-627A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-723-415B-6
                                                                                                                                                                                                                                                                                                                                  US-09-189-627A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC COMPANIAL SYSTEM: PC COMPANIAL SYSTEM: PC-DOS/MS-DOS SOFTMARE: PATENTIN PALEASE #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/723.41**
FILING DATE: 30-SPR.11-11**
CLASSIFT...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.8%;
Best Local Similarity 97.3%;
Matches 36; Conservative
                                                 SEQ ID NO 6
                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09189627A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: GB 9610195.1
PILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: CTAVEOID, AITHUI R.
REGISTRATION NUMBER: 25.327
REFERENCE/DOCKET NUMBER: 117-220
                                                                                                                                                                                                                                                                                 ENERAL INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPAX: 703-815-4100
FORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                     102 ENIRRRYYDALNYLMAMNIISKEKKEIKWIGLPTNSA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: NIXON
STREET: 1100 NO.
CITY: Arlington
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                       1 KNIRRRYYDALHYLAMNIISKEKKEIKWIGLPINSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
2IP: 22201-4741
                                                 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                              La Thangue, Nicholas
de la Luna, Susans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1100 NO. 5859199th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                         MBER: GB 9610195
                                                                                                                                                                                                                                 TRANSCRIPTION FACTOR DP-3 AND ISOPORMS THEREOF
                                                                                                                                                                               MERT: US/09/189,627A
1948-13-10
                                                                                                                                                            08/723,415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 182; DB 2;
Pred. No. 8.48-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 370;
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Page 6
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Search completed: August 28, 2002, 12:59:33
Job time: 144 sec
                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein . US-08-723-4158-8
                                                                                                                                                                 Overy Match 97.8%; Score 182; DB 2; UBest Local Similarity 97.3%; Pred. No. 8.8e-20; Matches 36; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 22201-4741

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release $1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION MINBER: US/08/723,415B
FILING DATE: 30-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: NIXON & VANDERHYE P.C.
STREET; 1100 No. 5859199th Glebe Rd. 8th floox
CITY: Arlington
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAL INPORMATION:
PLICANT: LaThangue, Nicholas B.
PLICANT: deLaluna, Susans
TLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
TLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFERENCE/DOCKET NUMBER: 117-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLICATION NUMBER: GB 9610195.1 TLING DATE: 15-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ee 8, Application US/087234158 No. 5859199
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                               OR SEQ ID NO: 8:
HARACTERAXORYSC:
385 amino acids
                                                                                                                                                                                                        Length 385;
                                                                                                                                                                     Indels
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Run on:

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Title:
Perfect score:
Sequence:
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Listing first 45 summaries
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score greater than or equal to the score of the result being printed
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
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186
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNIRRVYDALNVLMAMNIISKEKKEIKWIGLPINSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/BCOMB.COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 4.5
(c) 1993 - 2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search time 12.99 Seconds (without alignments) 69.573 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                    Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-308-935-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 18
SOFTHARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 37
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                         Query Match

Best Local Similarity 100.0%; i
Matches 37; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6268334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NOMBER: US/09/108,915
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: PC7/GB97/03506
EARLIER FILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: GB 9626589.7
EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICART: Bandara, Lasantha R
TITLE OF INVENTION: Peptide entagonists of DP
FILE REFERENCE: 620-67
                                                                         TITLE OF INVENTION: TINUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                     ADDRESSEE:
STREET: 1
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                            1 KNIRRRYTDALNYJAUDNI SKEKKEIKMIGLPTNSA 37
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                                                                                                                                                                                                                       cains ost
                                         1100 No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thangue, Nicholas B
                                                                                                            LA Thangue, Nicholas Barrie
VENTION: Transcription Factor DP-1
                                       Nixon & Vanderhye
00 No. 3863757th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                           Score 186; D8 4; Pred. No. 1.3e-21; Pred. No. 1.3e-21;
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                                                                                                                                                                                                                                                                                                                                                                                           Length 37;
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Indels

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Gaps

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Result

Minimum DB

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Query Natch 100. Best Local Similarity 100. Marches 37, Conservative
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,596
FILING DATE:
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
                                              APPLICATION NOWBER: US/08/428/131
FILING DATE: 23-JUN-1995
INTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-181
                                                                                                                                                    RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
              ELECOMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 KNIRRRYDALNYLMANNIISKEKKEIKHIGLPINSA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KNIRRRYTAALMYLJAJNIISKEKKEIKWIGLPINSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ICANT: La Thangue, Nicholas Barria
E OF INVENTION: Transcription Factor DP-1
ER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGTH: (72 amino acids)
PE: Amino acid
RANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPUTER: IBM PC compatible ERATING STOTEM: PC-DOS/NS-DOS PTHANE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/090785
                                                                                                                                                                                                                                                                                                                                                                                                       1100 No. 6150116th Glabe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703) 816-4000
(703) 816-4100
OR SEO ID NO: 11-
(703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 - JUN- 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and stands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 186; DB 2
100.0%; Pred. No. 3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/428, 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wisma tches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>..</u>
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; TOPOLOGY: linear; HOLECULE TYPE; protein US-08-723-4198-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-078-596-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                  NAME: CIRWFORD, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PATENTIN Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: GB 9610195.1
                                                                                                                                                                    STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/723,4158 FILING DATE: 30-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KNIRRRVYDALNVLMAMNIISKEKKEIKWIGLPINSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               watch Match D0.0%; Score 186; D8 4; Length 72; Local Similarity 100.0%; Pred. No. 3e-21; Concervative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 KHIRRYYDALNYLMAMNIISKEKKEIKHIGLPINSA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOPORMS
E OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08723415B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2: NIXON & VANDERHYB P.C.
1100 No. 5859199th Glebe Rd. 8th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LaThangue, Nicholas B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Release #1.0, Version #1.30
Score 186; DB 2;
Pred. No. 2.3e-20;
Nismatches 0;
                                                                                                                                                                                                                                                                                                                                         117-220
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Sequence 11, Application US/08723415B

Local Similarity 100.0%; Local Similarity 100.0%; les 37; Conservative 0;

<u>..</u>

Length 410; Indels

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CONFUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC.COS/MS-COS
SOPTWARE: PSIGNIF RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION MUMBER: US/08/723,4159
FILING DATE: 13-WAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: GB 9610195.1
PILING DATE: 15-WAY-1996
ATTORNEY/AGBAT INFORMATION:
NAMPLICATION TO ANTI-ED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 100.0%; Score 186; DB 2; Best Local Similarity 100.0%; Pred. No. 2.3e-20; Vatches 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                            08-428-131-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 703-816-4100
NFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                     COUNTRY: U.S.A.

IIP: 2201-4714
COMPUTER READABLE FORM:
REDUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE_COCKET NUMBER: 117-220
FELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                      APPLICANT: La Thengue, Micholas Barrie
FITLE OF INVENTION: Transcription Factor DP-1
TUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear HOLECULE TYPE: protein
                                                                                                                                                       STREET: 1100 NG
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITLE OF INVENTION: TRANSCRIPTION FACTOR OP-3 AND ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NO. 5859199th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 410 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                       RRESPONDENCE ADDRESS

    Application US/08428131
    5863757

                                                                                                                                                                                            1100 No. 5863757th Glabe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LaThangue, Micholas B.
deLaluna, Susana
    Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-602-846-2
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                                                                                                      WOLECULE TYPE: protein
Overy Match 100.0%; Score 186; DB; Best Local Smilarity 100.0%; Pred. Mo 2.3e-20; Matches 37; Conservative 0; Mismatches 0.
                                                                                                                                                       TELEFA: (703) 815-4100
INFORMATION FOR SED ID NO: 2:
SECOUNCE CHARACTERISTICS:
LENGTH: 410 maino acids
TYPE: maino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PATENTI Release 41.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR R.
RECISTRATION NUMBER: 25,337
REFERENCE/DOCKET NUMBER: 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                     TELECONMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 KNIRRYYDALNYLMANIISKEKKEIKWIGLPTHSA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Arthur R. Crawford
REGIESTRATION MUMBER: 25,327
REFERENCE/DOCKET MUMBER: 117-
ELECOMMUNICATION INFORMATION:
TELEPHOME: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Application US/08602846 5871901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               410 amino acids
                                                                                                                                                                                                                                                                                                                        620-12
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Query Match 100.0%; Score 186; DB 3; Best Local Similarity 100.0%; Pred. No. 2.3e-20; Matches 37; Conservative 0; Mismatches 0;
1 KNIRRRYTDALNYLAAMNIISKEKKEIRWIGLPTNSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NOWBER: US/09/428,131 FILING DATE: 23-JUN-1995
                                                                                                                   Length 410;
                                                                   Indels . 0:
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LICANT: LA Thangue, Micholas B LE OF INVENTION: ASSAY FOR INHIBITORS OF DP-1 AND OTHER DP LE OF INVENTION: PROTEINS. Bith Ploor, 1100 No. 5871901th Glebe Road US/08/602, 846

Length 410;

Indels

0

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US-09-078-596-2
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Best Local Similarity 100.
Atches 37; Conservative
                                                                                                                                                                                                                                                                           09-189-627A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: (703) 816-4100
INFORMATION FOR SEC ID NO: (3
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
PLICANT: LA Thangue, NICholas

PLICANT: de la Luna, Susana
TLE OF INVENTION TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
LE REFERENCE: 620-54
RREHT APPLICATION NUMBER: US/09/189,627A
RREHT FILING DATE: 198-11-10
IOR APPLICATION NUMBER: 08/723,415
IOR APPLICATION NUMBER: 08/723,415
IOR APPLICATION NUMBER: 08/723,415
IOR APPLICATION NUMBER: 08/723,415
IOR FILING DATE: 1986-09-30
IOR APPLICATION NUMBER: 08/723,415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CUREENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0
FILING DATE: 23-JUN-1995
TORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/078,596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNIRRRYTDALHYLMAMIISKEKKEIKWIGLPTNSA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arlington : Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 410 amino acida
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application 05/09078596
                                                                                                                                                                                                                                                    Application US/09189627A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2: Nixon & Vanderhye
1100 No. 6150116th Glebe Road, Bth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    La Thangue, Nicholas Barrie
ENTION: Transcription Factor DP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 186; DB 4; Length 410; 100.0%; Pred. No. 2.3e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/428, 131
                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-189-627A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : ORGANISM: human
US-09-189-627A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE, 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-189-627A-11
                                                                                                                                                                                                                                                                                                                                                  Hence 4, Application of No. 5859199
NERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 KNIRRRYYDALNYLMANNIISKEKKEIKNIGLPTNSA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KNIRRRYYDALNYLJUMNIISKEKKEIKWIGLPINSA 37
                                                           EDION TYPE: Ploppy
                                                                                                                                                                                                   DDRESSEB:
                                                                                                                                                                                                                                                                                  INVENTION: TRANSCRIPTION PACTOR DP-3 AND ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                         Application US/08723415B
                                                                                                                                                                                 B: NIXON & VANDERHYE P.C.
1100 No. 5859199th Glebe Rd.
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100.0%; Score 186; DB 4; 100.0%; Pred. No. 2.3e-20;

Length 410;

Indels

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Opps Bde3

Nicholas 8.

8th floor

PC-DOS/MS-DOS

Release #1.0, Version #1.30

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Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                     163 KNIRRVYDALNVLMAMNIISKEKKEIKNIGLPTHSA 199
                                                                                                                                                                                                                                                                                                        1 KNIRRRYYDALNYLMANNIISKEKKEIKWIGLPINSA 37
                                                              APPLICATION NUMBER: US/09/189,627A FILING DATE: 1998-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Ver. 2.0
                                                                                                                                  La Thangue, Nicholas
de la Luna, Susana
                                                                                                                                                                                                  Application US/09189627A
                                                                                                                                                                                                                                                                                                                                                         Conservative
1996-05-15
                                06-60-9661
                                                                                                                 TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 186; DB 4;
100.0%; Pred. No. 2.3e-20;
               GB 9610195.
                                               08/723,415
                                                                                                                                                                                                                                                                                                                                                                                        Cength 410,
                                                                                                                                                                                                                                                                                                                                                         Indels
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P
B
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APPLICATION NUMBER:

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US-09-189-627A-4
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Best Local Similarity 97.3%;
Matches 36; Conservative
                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-189-627A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                         O) ENTRERVYDALNVLMAMNIISKEKKEIKWIGLPTNSA 137
                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ME: Crawford, Arthur R. GISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICATION NUMBER:
ILING DATE: 1996-
                                                                                                                                                                                                               36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/189,627A
FILING DATE: 1998-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09189627A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      La Thangue, Nicholas
de la Luna, Susana
                                                                           pplication US/08723415B
59199
LaThangue, Nicholas B.
deLaluna, Susana
TENTION: THERBOP

ENTION: THERBOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DH: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF 620-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: US/08/723,415B
30-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                       1996-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                      1996-09-30
                                                                                                                                                                                                                           97.8%; Score 182; DB 4; 97.3%; Pred. No. 8.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB 9610195.1
                                                                                                                                                                                                                                                                                                                                                                                                       GB 9610195
                                                                                                                                                                                                                                                                                                                                                                                                                                  08/723,415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 182; DB 2;
Pred. No. 8.4e-20;
1; Mismatches 0
                                                                                                                                                                                                                                         DB 4; Length 369;
                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 369;
                                                                                                                                                                                                               Indels
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Query Match
Best Local Similarity
Matches 36; Conserv
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MEDION TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                   LICANT: Le Thengue, Nicholas
LICANT: de la Luna, Susana
LE OF INVENTION: TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/723,419B
FILING DATE: 30-SEP-1996
370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                              Application US/09189627A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: NIXON & VANDERBYE P.C.
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patentin Release $1.0, Version $1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                 1996-09-30
                                                                                                                                                                                                                                                                                                                                                                            97.8%;
97.3%;
                                                                                                                                                        RANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB 9610195.1
                                                                                                                           US/09/189, 627A
                                                                    GB 9610195
                                                                                                                                                                                                                                                                                                                                                                          Score 182; DB 2;
Pred. No. 8.4e-20;
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Query Match

Best Local Similarity 97.

Matches 36; Conservative

; Score 182; DB ; Pred. No. 8.4e 1; Mismatches

DB 4; Length 370;

Indels

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us-09-900-147-1.rai
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; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-08-723-4158-8
                                                                            Justy Match 97.8%; Score 182; DB 2; L est Local Similarity 97.3%; Pred. No. 8.8e-20; Matches 36; Conservative 1; Mismatches 0;
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IT: 22201-4741

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOSTWARE: Patentin Release $1.0. Version $1.30

CURRENT APPLICATION DATA:

APPLICATION MUMBER: US/08/723.415B

FILING DATE: 30-SEP-1996

CLASSIFICATION MUMBER: GB 9610195.1

FILING DATE: 15-MAY-1996

ATTORNETY AGENT INFORMATION:

NAME: CTRAFORD, ARTHUR R.

RESERVENCE CONCEPT WINDER: 25.327

RESERVENCE CONCEPT WINDER: 25.327
TREET: 1100 No.
ITY: Arlington
TATE: VA
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1100 No. 5859199th Glebe Rd.
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                                                                                                                   Length 385;
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Search completed: August 28, 2002, 12:59:33 Job time: 144 sec

Page 6